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Genome-wide association analysis for quantitative trait loci influencing Warner–Bratzler shear force in five taurine cattle breeds

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Summary

We performed a genome-wide association study for Warner–Bratzler shear force (WBSF), a measure of meat tenderness, by genotyping 3360 animals from five breeds with 54 790 BovineSNP50 and 96 putative single-nucleotide polymorphisms (SNPs) within *μ-calpain* [HUGO nomenclature *calpain 1, (mu/I) large subunit; CAPN1*] and *calpastatin* (*CAST*). Within- and across-breed analyses estimated SNP allele substitution effects (ASEs) by genomic best linear unbiased prediction (GBLUP) and variance components by restricted maximum likelihood under an animal model incorporating a genomic relationship matrix. GBLUP estimates of ASEs from the across-breed analysis were moderately correlated (0.31–0.66) with those from the individual within-breed analyses, indicating that prediction equations for molecular estimates of breeding value developed from across-breed analyses should be effective for genomic selection within breeds. We identified 79 genomic regions associated with WBSF in at least three breeds, but only eight were detected in all five breeds, suggesting that the within-breed analyses were underpowered, that different quantitative trait loci (QTL) underlie variation between breeds or that the BovineSNP50 SNP density is insufficient to detect common QTL among breeds. In the across-breed analysis, *CAPN1* was followed by *CAST* as the most strongly associated WBSF QTL genome-wide, and associations with both were detected in all five breeds. We show that none of the four commercialized *CAST* and *CAPN1* SNP diagnostics are causal for associations with WBSF, and we putatively fine-map the *CAPN1* causal mutation to a 4581-bp region. We estimate that variation in *CAST* and *CAPN1* explains 1.02 and 1.85% of the phenotypic variation in WBSF respectively.

Keywords beef, *Bos taurus taurus*, calpain 1, (mu/I) large subunit, calpastatin, genome-wide association, haplotype, meat tenderness, quantitative trait loci, single-nucleotide polymorphisms, Warner–Bratzler shear force.

Introduction

Consumer assessment of beef quality, palatability and overall eating satisfaction is significantly influenced by tenderness (Huffman *et al.* 1996; Weston *et al.* 2002;

Moser *et al.* 2004; Smith *et al.* 2006), and consumers have indicated a willingness to pay a premium for 'guaranteed tender' steak (Boleman *et al.* 1997; Mintert *et al.* 2000; Miller *et al.* 2001; Platter *et al.* 2005). Inadequate tenderness has consistently been identified in National Beef Quality Audits as a priority quality challenge (Lorenzen *et al.* 1993; Roeber *et al.* 2000; Shook *et al.* 2008) because consumers consider tenderness to be the single most important component of meat quality and will substitute protein sources motivated by their dissatisfaction from the purchase of a tough cut (Miller *et al.* 1995; McKenna *et al.* 2002).

To address these concerns, researchers have identified quantitative trait loci (QTL) for Warner–Bratzler shear

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force (WBSF) measurements on the longissimus dorsi muscle on chromosomes 2, 4, 5, 7, 10, 11, 15, 20, 25 and 29 (Casas *et al.* 1998, 2000, 2001, 2003; Keele *et al.* 1999; Rexroad *et al.* 2001; Alexander *et al.* 2007; Davis *et al.* 2008; Gutierrez-Gil *et al.* 2008; Gill *et al.* 2009, 2010). However, from these reported QTL, DNA marker tests have been developed and commercialized only from *calpastatin* (CAST) on chromosome 7 and *calpain 1, (mu/I) large subunit* (CAPN1) on chromosome 29 (Page *et al.* 2002, 2004; White *et al.* 2005; Casas *et al.* 2006; Van Eenennaam *et al.* 2007). While these commercialized marker tests are predictive of tenderness in both *Bos taurus* and *B. t. indicus* breeds, it appears that they are not causal for the detected associations with tenderness (Casas *et al.* 2003). However, the estimated genotypic associations estimated for these markers are large, with an average difference of 0.15 kg in WBSF between alternate homozygotes in independent studies involving several breeds (Casas *et al.* 2006; Morris *et al.* 2006; Van Eenennaam *et al.* 2007; Johnston & Graser 2010). While positional candidate genes on other chromosomes have been investigated (Rexroad *et al.* 2001; Stone *et al.* 2005), none have resulted in commercial tests.

To assist beef breeders to make efficient and large changes in tenderness, DNA assays must be developed that can reliably predict the genetic variation in tenderness without regard to the breed composition of an animal. To address this need, we genotyped 3360 animals representing 114 half-sib families produced by the American Angus Association (AAA), American Hereford Association (AHA), American Simmental Association (ASA), American International Charolais Association (AICA) and the North American Limousin Foundation (NALF) as part of the National Cattlemen's Beef Association (NCBA) sponsored Carcass Merit Project (CMP) to develop prediction equations for the implementation of genomic selection (Meuwissen *et al.* 2001) and to identify genomic regions associated with tenderness. This study reports genomic regions detected as being concordant across breeds, which putatively harbour candidate genes that influence tenderness and which could be targeted for the development of diagnostic assays. We also dissect variation within CAST and CAPN1 in order to identify the genomic regions most likely to harbour the causal variants influencing beef tenderness.

Materials and methods

Animals and phenotype

A total of 3360 animals representing five of the breed associations participating in the NCBA-sponsored CMP were selected for genotyping based on the availability of WBSF data and DNA samples (Table 1). The design of the CMP project has previously been described by Minick *et al.*

(2004); however, only the Angus and Hereford samples represent purebred populations, with the Continental breeds being represented by crossbred progeny, with Simmental, Charolais and Limousin sires mated to predominantly commercial Angus cows. Meat tenderness was measured as WBSF (kg) of longissimus dorsi steaks at day 14 post-mortem as previously described (Wheeler *et al.* 1998; Minick *et al.* 2004). Muscle samples, extracted DNA samples and carcass phenotypes produced in the CMP and owned by the AAA, AHA, ASA, AICA and NALF were transferred to the University of Missouri. All CMP animals had blood samples drawn at weaning, from which DNA was extracted and tested to validate the identity of their sires. Additionally, a muscle sample was taken at slaughter at the capture of phenotype data on most of the animals, and DNA extracted from a subset of the muscle samples was previously genotyped and compared with the genotype profiles produced from the corresponding blood samples to validate the identity of each carcass. This process identified that about 10% of animals or carcasses were misidentified (Thallman *et al.* 2003) likely due to changes in the order of carcasses because of 'rail-outs' at packing plants. To resolve this issue, we extracted genomic DNA from 2940 muscle samples taken from the phenotyped carcasses by proteinase K digestion followed by phenol-chloroform-isoamyl alcohol extraction and ethanol precipitation (Sambrook *et al.* 1989). The remaining 420 DNA samples were extracted from the blood, but these samples had previously been DNA-typed and successfully matched to the sample taken at harvest.

Genotypes

All samples were genotyped using the Illumina BovineSNP50 BeadArray (Matukumalli *et al.* 2009) for 54 790 single-nucleotide polymorphisms (SNPs) and a custom-designed Illumina GoldenGate assay incorporating 96 putative SNPs located within 186 kb of CAST and CAPN1 (Table S1), discovered either as part of the bovine genome sequencing project or through directed CAPN1 resequencing studies at the US Meat Animal Research Center at Clay

Table 1 Animal counts, mean phenotype and estimates of additive genetic variance and heritability by breed.

Breed	Count		Warner-Bratzler shear force (kg)		
	Animals ¹	Sires	Average	σ_A^2	h^2
Angus	660 (651)	20	3.74	0.22	0.52
Charolais	702 (695)	18	4.41	0.23	0.46
Hereford	1192 (1095)	29	4.75	0.15	0.17
Limousin	285 (283)	23	4.28	0.07	0.09
Simmental	521 (516)	24	4.36	0.06	0.08
All Breeds	3360 (3240)	114	4.37	0.17	0.25

¹Numbers of animals with genotype call rate ≥ 0.85 in parentheses.

Center, NE (Page *et al.* 2002; White *et al.* 2005; Casas *et al.* 2006). Several of the putative SNPs identified in the genome sequencing project were not variable (Table S1), and we were much more successful in fine-mapping *CAPN1* than *CAST*. All genotypes were called in the Illumina GENOMESTUDIO software. Genotypes were filtered according to their unique localization to an autosome or the X chromosome in the University of Maryland sequence assembly (UMD3.0; Zimin *et al.* 2009), call rate (>0.89) and minor allele frequency >0.01 within each breed. Animals were excluded if their individual genotype call rate was <0.85 . The call rate of >0.89 for SNP filtering was used to ensure that all commercialized tenderness SNPs were included in the analysis. After filtering, the data set comprised 40 645 SNPs assayed in 3240 animals (Tables 1 and S2).

Analysis

FASTPHASE v1.2.3 (Scheet & Stephens 2006) was used with UMD3.0 coordinates to phase all genotypes and impute the 0.89% of missing genotypes. The complete set of genotypes was then used to generate a genomic relationship matrix (G) across all breeds using the first of the methods described by VanRaden (2008) with a modification allowing the inclusion of X-linked loci as described below.

Warner–Bratzler shear force phenotypes were analysed under a single-trait mixed linear animal model in which the genomic relationship matrix was used to represent the realized identity by descent among the animals. The model fit was $y = X\beta + Zu + e$ where y is a vector of WBSF measurements, β is a vector of fixed contemporary group effects defined as breed \times herd of origin \times sex of calf \times slaughter date, u is a vector of random additive genetic merits, and e is a vector of random residuals. The matrices X and Z are incidence matrices relating observations to levels of the fixed and random effects, and we assume that $\text{Var}(u) = G\sigma_A^2$, $\text{Var}(e) = I\sigma_E^2$ and $\text{Cov}(u, e) = 0$. Restricted maximum likelihood was used to estimate the variance components σ_A^2 and σ_E^2 and iteration on the variance component estimates continued until the estimate of heritability $h^2 = \sigma_A^2 / (\sigma_A^2 + \sigma_E^2)$ had converged to four significant figures. At convergence, the GBLUP of the vector of SNP allele substitution effects (ASEs) was obtained as $\hat{a} = (2\sum_i p_i q_i)^{-1} M'G^{-1} \hat{u}$ where p_i is the frequency of the A allele at the i th SNP (genotypes at each SNP are called in A/B space by the GenomeStudio software), $q_i = 1 - p_i$, elements of the i th column of M are $2q_i$, $q_i - p_i$ and $-2p_i$ for AA , AB and BB genotypes at autosomal and pseudoautosomal loci (VanRaden 2008) and are q_i and $-p_i$ for AY and BY genotypes at X-linked loci in males, and \hat{u} is GBLUP of u . Analyses were performed both within each breed and across all breeds.

The variance component associated with SNP ASEs is $\sigma_M^2 = (2\sum_i p_i q_i)^{-1} \sigma_A^2$, and for each SNP, the predicted ASE was normalized to a t -like statistic as $t_i = |\alpha_i| / \sigma_M$. These

values are included in Table S2 and are shown in the Manhattan plots in Figs 1 and S1.

Across-breed comparison of putative QTL regions

To determine whether common QTL influence WBSF across breeds, we ranked the t_i values estimated in the within- and across-breed analyses and then identified SNPs for which the t_i values ranked in the top 500 (1.2%) of SNP ASEs in the across-breed analysis. For each of the regions tagged by these SNPs, we declared the region to harbour a QTL if at least three SNPs from different within-breed analyses had ASEs ranked in the top 500. While linkage disequilibrium (LD) decays to ~ 0.1 within less than a 500-kb distance within breeds of distantly related individuals (McKay *et al.* 2007), many of the individuals incorporated into these analyses are half-sibs (Table 1), which leads to a much greater extent of LD because of large common chromosomal segments transmitted by the sires to their progeny. Additionally, we wanted to allow for the possibility that more than one QTL could be present within any one genomic region. Accordingly, we allowed the region size to vary up to 5.7 Mb (average 1.7 Mb) as determined by the signatures of the detected within-breed SNP ASE ranks. Furthermore, within each region, we did not expect to find the same SNP to be most strongly associated with WBSF, because differences in SNP and QTL allele frequencies between breeds (Table S2) can lead to different patterns of LD in different breeds.

Candidate genes

Genomic regions identified as being associated with WBSF in at least four breeds were analysed using the NCBI

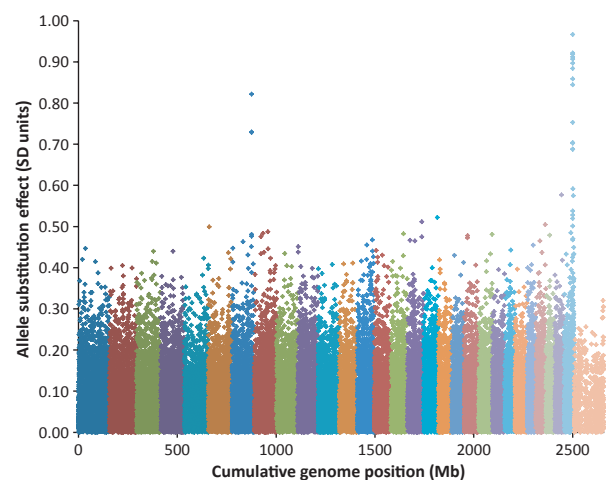


Figure 1 Manhattan plot of single-nucleotide polymorphism (SNP) allele substitution effects estimated in the across-breed analysis and normalized by the square root of the estimated SNP variance component.

Entrez Map Viewer (accessed 07/06/2011) to identify potential candidate genes for tenderness.

CAST and CAPN1

A 1.48-Mb region of BTA7 harbouring 28 SNPs spanning *CAST* and a 2.64-Mb region of BTA29 harbouring 93 SNPs spanning *CAPN1* were found to contain loci for which SNP ASEs ranked in the top 500 in the within-breed analyses. To allow haplotype-based analyses, we expanded the regions to 44 SNPs spanning 2.86 Mb for *CAST* and 100 SNPs spanning 3.12 Mb for *CAPN1* (Table S3). We first analysed each SNP individually by including allele effects (the difference between the two estimated allele effects is the ASE for the SNP) in β , in addition to the contemporary group effects, and then we included haplotype effects for windows of nine contiguous SNPs using phase information estimated by *FASTPHASE*. The haplotype model was sequentially fit by sliding the nine SNP window through each region one SNP at a time, and the statistics computed for each window were assigned to the 5th SNP located at the centre of each window. In both cases, the analysis was performed using the previously estimated variance components (Table 1), and *F*-tests for SNP or haplotype effects were constructed from the difference between model sums of squares including and excluding the fitted SNP or haplotype effects, the difference in number of parameters between the fitted models and the estimated residual variance for the full model. Because the number of detected haplotypes varied throughout each region (Table S3), the window producing the largest model sum of squares does not necessarily result in the largest *F*-statistic or $-\log_{10}P$ -value (because the numerator mean square can be significantly influenced when its degrees of freedom are small but vary between tests). To avoid this, we computed the percentage of phenotypic variation explained by each window through the region from the ratio of the window to phenotypic sums of squares, where the window sum of squares was estimated as the difference between model sum of squares including and excluding haplotype effects for the nine SNP window and the phenotypic sum of squares was estimated as the total sum of squares corrected for the mean and contemporary group sums of squares. This statistic identifies the SNP window that explains the largest amount of variation in WBSF regardless of the number of haplotypes that are fit.

Results and discussion

We found large differences in the heritabilities of WBSF across the five breeds (Table 1) and were concerned that this might reflect differences in data quality or the correct assignment of phenotype to genotype because of the sample misidentification issue identified within the CMP. However, we also estimated heritabilities for eight additional

carcass traits recorded in this project (data not shown) and found no evidence for systematically lower heritabilities within any of the breeds. We therefore conclude that the re-extraction of DNA from tissue samples taken from the carcass at slaughter effectively solved the misidentification problem. Thus, the variation in heritabilities probably reflects the relatively small sample size within each breed and the sampling of the bulls used to produce these animals. However, the effect of variation in heritability across breeds was to substantially influence the 'genetic' sample size which we estimate as $N \times h$, the number of phenotypes multiplied by the square root of the heritability, which is an estimate of the cumulative amount of additive genetic information in a sample of N unrelated individuals and was 468.3, 451.5, 471.7, 85.4 and 143.5 in Angus, Hereford, Charolais, Limousin and Simmental respectively.

In the across-breed analysis, the use of the genomic relationship matrix corrects for the stratification because of pedigree relatedness while accounting for the extent of background relatedness among the Angus and Continental breed groups because of the use of Angus dams to produce the crossbred Continental breed calves. In this analysis, the associations between the *CAST* and *CAPN1* loci with WBSF were the largest in the genome (Fig. 1), reflecting both the magnitude of effects of these genes and the increased SNP density within these regions, which improves the likelihood of finding SNP in strong LD with the causal mutations. The within-breed analyses identified *CAPN1* as the locus most strongly associated with WBSF genome-wide, although the highest ranked SNP ASE within this region for Limousin was only 30th (Table S2), presumably reflecting the very small sample size for this breed. On the other hand, the *CAST* associations were more variable among the breeds, being the most strongly associated with WBSF genome-wide in Hereford, ranking highly in Charolais and Limousin, but only 234th and 208th in Angus and Simmental respectively. These results are likely due to the fairly small sample sizes for the analysed breeds, but probably also may reflect the different SNP densities within the two regions and differences in allele frequencies at the SNPs and QTL across breeds. We accomplished a much higher SNP density in the region harbouring *CAPN1* than *CAST*, and this suggests that we had insufficient SNPs to find at least one that was in strong LD with the causal mutations within *CAST* in all breeds.

Across all 40 645 SNPs, the correlations between ASEs estimated within each of the breeds varied from -0.02 to 0.04 , indicating that models developed to predict genomic breeding values within one breed will have very low accuracies in other breeds. This has previously been predicted using simulated data (de Roos *et al.* 2009; Toosi *et al.* 2010) but, despite the use of commercial Angus females to produce the Continental breed crossbred steers, it is a

consequence of the genetic distance between the training and validation sets of animals. Habier *et al.* (2010) demonstrated that the number of generations that separate the training and validation data sets influences the accuracy of genomic breeding values estimated in the validation set, with lower accuracies occurring when this relationship is more distant. On the other hand, the correlations between the ASEs estimated in the across-breed analysis and those estimated in the within-breed analyses were 0.37, 0.66, 0.41, 0.31 and 0.42 for Angus, Hereford, Charolais, Limousin and Simmental respectively. This result supports the simulation results of Toosi *et al.* (2010), who showed that training in admixed populations results in genomic estimates of breeding value with accuracies almost equivalent to those achieved from training and validating within the same breed. Of course, the key benefits from the perspective of beef cattle breeding are that training population samples can dramatically be increased by pooling breeds and that the resulting genomic breeding values have industry-wide utility.

Hayes & Goddard (2001) have estimated that between 50 and 100 QTL underlie variation in quantitative traits within livestock populations. While under neutral theory, the common QTL mutations that are detectable by GWA analysis must predate the domestication of cattle (Kimura & Ohta 1973), the relatively small populations upon which breeds were founded may have led to the sampling of different subsets of QTL within different breeds. In fact, the extent to which breeds share common QTL is unknown (Pryce *et al.* 2010), but is of some importance to the development of prediction equations for molecular estimates of breeding value in admixed populations and the development and utilization of genotyping assays for the prediction of genetic merit within the beef industry. To identify QTL underlying variation in WBSF, we examined the genomic regions harbouring the 500 SNPs with the largest ASEs from the across-breed analysis for SNPs with ASEs ranked in the top 500 in the within-breed analyses for at least three of the breeds. We identified 79 genomic regions that putatively harbour QTL influencing WBSF (Table 2). Of these, 42 were identified in three breeds, 29 in four breeds and eight in all five breeds. There was no difference between the breeds ($P = 0.48$) or between British and Continental breeds ($P = 0.52$) in the probability of QTL detection for all 79 QTL or for the 42 QTL identified in only three breeds ($P = 0.35$ and 0.82 respectively). Clearly sample size, assay SNP density, constraints on SNP ranks and the size of regions harbouring highly ranked SNP ASEs all impact the identification of putatively common QTL. Of the 113 instances when the within-breed estimated SNP ASEs ranked >500 , the average rank was only 2551, suggesting that the majority of these regions harbour QTL that segregate in all breeds. Changing the minimum within-breed ASE rank criterion to <1000 resulted in 17 of these QTL being detected in all

five breeds, 41 in four breeds and 21 in three breeds (Table 2). Thus, there appears to be little phylogenetic signal in these data, and if a QTL was detected in only three breeds, these breeds were as likely to be British and Continental as strictly Continental.

We have previously found poor concordance between GWA and half-sib linkage analyses for large-effect QTL underlying growth traits, even when large numbers (>50) of families with family sizes ranging from 20 to 224 half-sibs are analysed (data not shown). Assuming that GWA analysis detects common variants, we would expect a significant number of sires to be both heterozygous and detected to be segregating for a large-effect QTL; however, this largely depends on the underlying genetic architecture of the trait. Reed *et al.* (2008) found that growth was affected in 34% of viable mouse knockouts, suggesting that natural variation in thousands of genes underlies variation in growth. As a consequence of this complex genetic architecture, there may be a large number of QTL on each chromosome, and the allelic combinations present at these QTL in the sire will impact on whether any one QTL is detected in linkage analyses. Thus, common variants detected in GWA analysis may not be detected in segregation analysis, and rare variants detected in segregation analysis may not be detected in GWA analysis. Nevertheless, we found six of the 12 previously reported meat tenderness QTL, including *CAST* and *CAPN1*, to coincide with the QTL identified in this study (Table 2) (Cattle QTL database, http://www.animalgenome.org/cgi-bin/QTLdb/BT/draw_traitmap?trait_ID=1030, accessed June 27, 2011). Notwithstanding the poor resolution of QTL location mapped by linkage analysis, we also found support for all of the other previously identified QTL. For example, in the across-breed analysis, QTL were identified with ASE ranks <500 at 3 151 989 bp and at 6 831 955–7 086 105 bp (300 kb from *MSTN*) on BTA2. The first was supported by ASE ranks <500 for Angus and Charolais, but an ASE rank of 565 in Limousin. The second was supported by an ASE rank <500 in Charolais and ASE ranks <1000 in Angus, Limousin and Simmental. Thus, despite their proximity, these QTL are likely distinct, and the concordance between our and previously published results suggests that the genetic architecture of meat tenderness is substantially less complex than for growth.

We examined the genomic regions harbouring the 37 QTL that were detected in at least four of the breeds for potential candidate genes underlying meat tenderness. Very little is known about the genetic regulation of meat tenderness, and few candidate genes are suggested for these QTL. While *CAST* and *CAPN1* have consistently been identified and analysed as candidate genes for the BTA7 97 861 341–98 820 742-bp and BTA29 44 042 363–44 087 629-bp QTL, respectively, no causal variants have been identified in either gene. *CAPN1*

Table 2 Genomic regions identified as harbouring QTL that were detected in at least three breeds.

BTA	Start ¹	End ¹	SNP ²	Location ²	No. SNP ³	Breeds	Angus ⁴	Hereford ⁴	Charolais ⁴	Limousin ⁴	Simmental ⁴	All breeds ⁴
1	27 034 490	29 073 969	rs42409195	28 111 487	30 (2)	C, L, S	7433	6333	37	189	19	335
1	155 725 361	156 105 357	rs41600022	155 725 361	8 (1)	H, L, S	2242	43	967	429	267	423
3	306 322	1 267 869	ss86301348	1 267 869	17 (1)	A, H, C	154	134	222	6584	3319	210
4	62 189 085	62 766 267	rs43403458	62 685 650	16 (2)	H, C, S	2695	244	292	1679	176	60
5	4 501 932	5 240 327	ss86306901*	5 012 505	15 (1)	A, H, S	90	422	8827	3688	453	458
5	21 876 606	23 103 768	rs29014779	21 876 606	19 (1)	C, L, S	846	3002	51	441	181	444
5	99 077 991	101 271 357	rs41654473	101 271 357	24 (1)	C, L, S	1105	1269	83	280	270	319
6	20 730 690	22 576 164	rs42756258	21 884 446	36 (2)	A, C, L, S	10	2467	191	304	78	190
6	102 116 041	104 245 701	ss117968229	103 281 884	44 (3)	A, L, S	214	625	1463	94	48	273
7	55 116 289	57 554 684	rs29012174	55 116 289	36 (1)	A, H, L, S	65	132	727	105	262	47
7	73 155 944	74 367 220	ss86318554	74 367 220	28 (1)	A, H, C, L	358	102	470	144	3570	288
7	77 854 696	83 621 039	rs43527386	80 731 488	89 (3)	H, C, L, S	1478	94	420	219	424	71
7	97 861 341	98 820 742	rs41255587*	98 579 574	19 (8)	A, H, C, L, S	237	1	14	37	308	10
7	106 927 241	108 205 624	rs43531510	106 927 241	24 (2)	H, C, S	8668	163	49	972	306	98
8	3 830 280	4 955 143	rs41618019	4 955 143	19 (1)	A, H, S	137	57	534	9307	189	296
8	43 890 714	46 946 557	rs42312419	43 890 714	48 (1)	H, C, L, S	3561	208	16	410	126	31
8	65 338 177	69 622 989	ss117969253	68 894 735	68 (4)	A, H, C, L, S	156	85	198	240	90	29
8	97 684 074	98 861 495	ss86319219	98 746 331	16 (1)	A, H, C, L	31	181	238	141	4390	184
8	112 287 843	113 301 368	ss86338099	112 824 694	28 (2)	A, C, L, S	76	1615	123	369	235	330
9	36 960 364	40 088 647	rs41623216	38 252 618	41 (2)	H, L, S	1224	410	1033	126	151	188
10	6 871 209	8 514 821	ss86317616	7 830 003	26 (1)	A, L, S	299	2813	3578	238	99	338
10	15 413 589	16 985 300	ss86317957	16 326 848	34 (1)	A, H, L, S	383	128	4565	486	451	113
10	29 278 086	31 692 125	ss86305679	29 278 086	29 (1)	A, H, L, S	162	184	896	449	293	161
10	38 799 891	40 135 969	rs42412333	39 278 374	18 (4)	A, H, S	222	120	4536	1974	336	211
10	96 842 358	98 541 920	rs41590854	97 410 796	26 (1)	A, H, L	239	415	777	113	764	262
10	102 286 251	103 234 411	rs41596899	102 308 122	25 (3)	H, C, L, S	3577	393	184	103	103	160
11	1 214 856	1 963 074	ss86324631	1 214 865	21 (1)	H, C, L, S	10476	235	469	173	107	124
11	31 734 782	33 348 373	rs41606137	32 224 661	26 (3)	A, L, S	288	1652	1054	336	168	241
12	35 454 037	36 764 448	ss117970656	35 581 416	20 (3)	H, C, S	3094	50	489	4969	211	149
12	50 715 278	52 618 243	rs43699567	52 573 538	40 (1)	A, H, C, L, S	416	288	385	352	27	498
13	3 723 531	5 128 166	rs42862024	4 308 889	22 (2)	A, H, S	107	381	3033	2879	341	305
13	29 072 163	33 201 457	rs29011158	31 826 409	64 (2)	A, H, C, L, S	315	242	31	36	4	151
13	66 080 035	69 702 161	rs41631563	66 080 035	72 (14)	A, H, C, S	471	8	61	787	142	97
13	73 369 210	73 746 516	ss86338902	73 746 516	9 (1)	A, H, S	344	127	594	2950	130	283
13	75 018 157	76 078 033	ss86289318	76 042 839	24 (2)	A, C, S	41	773	65	1767	110	43
13	80 848 032	81 665 695	rs42630433	81 029 787	21 (3)	A, H, C, L	386	48	69	41	5004	75
14	18 732 660	20 347 849	rs41633333	18 756 025	32 (5)	A, H, C	293	414	87	573	2160	76
14	47 926 524	48 572 837	ss86299784	48 184 967	13 (1)	C, L, S	2191	871	301	195	109	302
14	62 549 674	63 827 753	ss86297726	63 213 438	24 (1)	A, H, C, L	352	301	97	275	1445	166
15	31 599 942	33 310 389	ss86291817	32 861 621	32 (4)	A, H, L	311	31	1527	243	553	162
15	34 682 617	36 817 688	rs41757680*	35 661 186	40 (1)	A, H, C, L, S	99	21	53	32	468	354
15	48 688 111	50 222 093	rs41582705	48 936 679	10 (1)	C, L, S	4718	5799	172	162	124	119
15	62 309 986	63 517 557	rs41621125	63 253 454	20 (1)	H, C, L	9112	77	109	444	3538	74

Table 2 (continued)

BTA	Start ¹	End ¹	SNP ²	Location ²	No. SNP ³	Breeds	Angus ⁴	Hereford ⁴	Charolais ⁴	Limousin ⁴	Simmental ⁴	All breeds ⁴
15	64 876 840	66 717 899	ss86314348	64 876 840	15 (1)	H, C, L, S	1137	42	20	84	92	32
15	81 655 317	82 875 229	ss86296417	82 768 398	25 (1)	H, C, L	626	152	80	122	1842	178
16	11 797 915	13 358 683	rs41623175	12 130 589	23 (2)	A, H, C, L	18	18	4	272	1145	44
16	17 070 345	19 313 882	ss86290236	18 059 649	19 (1)	A, C, L, S	334	2017	256	381	96	353
16	22 147 468	23 830 920	ss86329907	22 406 467	17 (1)	A, H, C	401	88	354	1452	1920	216
16	25 000 153	28 384 914	ss86291490	27 629 566	39 (4)	H, C, L, S	1089	166	19	234	37	148
16	71 968 734	72 962 506	rs41824081	72 165 897	20 (2)	H, C, L	6937	265	467	55	2353	25
17	34 429 947	37 201424	rs41626299	34 429 947	25 (1)	H, C, L, S	1866	131	391	420	479	195
17	63 049 154	64 637 527	ss86317522	63 049 154	29 (1)	A, C, L, S	205	1220	347	454	391	278
17	73 315 120	74 393 620	ss86339946	73 315 120	27 (1)	A, C, S	166	551	361	5105	22	403
18	4 723 911	6 440 525	ss86336538	4 723 911	32 (1)	A, L, S	333	580	3125	151	251	83
18	55 028 139	55 621 823	ss86310723	55 590 144	10 (1)	A, H, S	363	418	5999	2353	28	489
20	15 870 897	17 710 059	rs41933103	17 175 071	35 (3)	H, C, L	1892	44	52	320	1009	36
20	64 002 006	66 587 451	ss86335963*	66 105 424	51 (2)	A, C, L, S	142	831	273	295	261	206
21	33 764 430	34 810 865	rs29015146	34 165 847	19 (1)	A, H, S	378	397	2032	924	322	434
21	40 955 783	43 096 903	rs42503056	40 955 783	30 (1)	A, H, S	116	350	4015	2961	113	85
21	59 665 710	61 121 046	rs41585245	61 121 046	22 (3)	A, C, L	458	703	211	205	1790	67
21	68 152 356	68 965 986	ss86312849	68 846 429	17 (4)	H, C, L	2122	108	209	83	1796	33
23	48 537 019	49 094 579	rs41617911	48 856 081	16 (1)	A, C, L	89	2461	332	448	2831	329
25	1 160 378	2 105 645	ss117973580	1 919 606	21 (2)	A, L, S	215	1633	2777	387	478	116
25	14 683 151	15 752 362	ss86336453	15 752 362	23 (2)	A, C, L, S	96	1940	306	60	145	132
25	19 762 712	22 728 704	rs41572366	21 655 452	47 (2)	A, H, C, L, S	97	63	495	3	258	102
25	27 545 745	30 572 524	ss86283327*	29 485 851	48 (2)	A, H, C, L, S	57	499	99	102	68	49
26	12 580 311	14 127 433	ss86273489	13 293 856	27 (1)	A, H, S	27	107	4581	641	461	144
26	17 058 843	18 288 540	ss86287439	18 288 540	25 (2)	A, H, L, S	243	404	512	93	212	138
26	29 698 221	31 348 288	rs41646897	30 903 998	37 (1)	A, H, C, S	420	76	317	897	183	63
26	41 183 634	43 312 255	ss86282954	42 274 097	37 (2)	H, L, S	3947	23	701	256	445	388
27	3 343 936	6 388 642	rs29024621	3 909 806	24 (1)	A, H, L, S	275	80	2437	412	201	401
27	19 195 734	21 993 669	rs42118878	19 195 734	39 (4)	H, L, S	2323	323	538	192	42	35
27	34 978 041	36 054 950	ss86310277	35 372 600	21 (1)	A, H, C, S	304	425	149	1423	222	364
28	4 837 387	5 876 902	rs41612729	5 052 476	24 (3)	H, C, L, S	1466	317	438	117	233	280
28	31 700 004	34 066 383	ss86337100	33 570 352	33 (1)	A, H, L, S	39	138	3800	70	7	19
28	37 398 488	38 314 983	rs29013966	37 514 643	20 (1)	H, C, S	624	320	110	916	450	84
28	43 815 607	44 961 253	ss86283362	44 694 578	25 (1)	A, C, S	153	834	121	696	84	389
29	34 618 653	36 573 929	rs29022154	35 387 115	35 (2)	A, C, L, S	120	2258	276	35	87	129
29	44 042 363	44 087 629	rs42192703*	44 070 713	30 (18)	A, H, C, L, S	1	4	1	30	1	1

A, Angus; C, Charolais; H, Hereford; L, Limousin; S, Simmental; QTL, quantitative trait loci; SNP, single-nucleotide polymorphism.

¹UMD3.0 coordinates for the SNPs defining the boundaries of the SNP putatively harbouring the QTL.

²Identity and UMD3.0 coordinate of the most strongly associated SNP within the interval as determined in the across-breed analysis. QTL previously reported in the Cow QTL Database (http://www.animalgenome.org/cgi-bin/QTLdb/BT/draw_traitmap?trait_ID=1030) are indicated with asterisks.

³Number of SNPs within the interval. Number of SNPs within the region ranked in top 500 ASEs in the across-breed analysis in parentheses.

⁴Lowest rank for t_i value within the interval.

encodes the protease μ -calpain, which has been implicated in the proteolysis of muscle proteins during meat ageing (Smith *et al.* 2000), and *CAST* encodes calpastatin, which is an inhibitor of μ -calpain (Goll *et al.* 2003). Myogenic determination factor 1 is a transcription factor encoded by *MYOD1* and is expressed in skeletal muscle during myogenesis and regeneration. Variation in *MYOD1* has been suggested to affect its ability to influence the expression of muscle structural components (Rexroad *et al.* 2001), making it a candidate for the QTL at 34 682 617–36 817 688 bp on BTA15. Calpain-2 (m/II) large subunit (m-calpain) is a calcium-activated neutral protease encoded by *CAPN2* on BTA16 (25 000 153–28 384 914 bp). M-calpain activity has been associated with both meat tenderness and palatability measurements (Riley *et al.* 2003). Fibroblast growth factor 2 (*FGF2*) is an upstream regulator of heat shock protein B1 (*HSPB1*), which has been found to be negatively related to WBSF (Kim *et al.* 2011), making it a candidate for the 34 429 947–37 201 424-bp QTL on BTA17. *GSN* encodes gelsolin, a calcium-regulated protein that functions in both the assembly and disassembly of actin filaments, which are a component of the contractile apparatus in muscle cells and may underlie the BTA8 112 287 843–113 301 368-bp QTL. Finally, *CALM1* encodes calmodulin, a calcium-binding protein, which interacts with titin and mediates smooth muscle contraction, making it a candidate for the BTA10 102 286 251–103 234 411-bp QTL.

While the commercially tested *CAST* SNP *rs41255587* was the most strongly associated with WBSF in the across-breed analysis ($-\log_{10}P = 8.95$), it was only the most strongly associated *CAST* SNP within Hereford and Charolais, with stronger associations being detected for SNPs in the 5' upstream region in Angus, Limousin and Simmental (Table S3). In fact, the haplotype analysis moves the location of the most significantly associated SNP window 83.7 kb upstream of *rs41255587* to be centred on *rs43529872* ($-\log_{10}P = 8.78$), and this *CAST* window was found to explain the greatest amount of phenotypic variation in WBSF in the across-breed (1.02%; Table 3), Angus and Hereford analyses. The sign and magnitude of the ASE was consistent for *rs41255587* in all breeds except Limousin, and the haplotype analysis explained considerably more variation in WBSF than the single SNP analysis, indicating that either the causal variant is not among the tested polymorphisms or that there is more than one causal variant. Furthermore, the haplotype analyses move the most likely location of the causal mutation 5' of the commercially tested *CAST* SNP *rs41255587*, probably in the 678-kb region from 97 861 341–98 538 952 bp (Fig. 2). Clearly, additional fine-mapping is required to identify the number of mutations influencing WBSF that lie in the vicinity of *CAST* and their most likely locations.

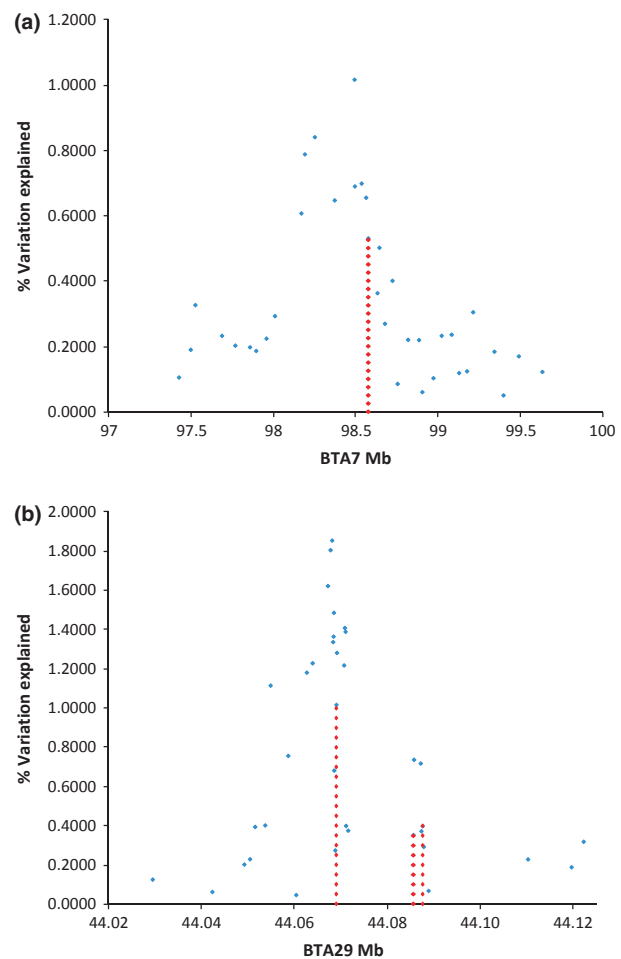


Figure 2 Proportion of phenotypic variation in the across-breed analysis explained by haplotypes constructed from nine consecutive single-nucleotide polymorphism (SNPs) in the region of (a) BTA7 harbouring *CAST* and (b) BTA29 harbouring *CAPN1*. Locations and amount of variation explained by the commercialized tenderness SNPs are indicated by red dotted lines.

Among the SNP located within *CAPN1*, *rs17812000* (c.316G>A) was most strongly associated with WBSF in Angus ($-\log_{10}P = 9.70$) and *rs17872050* was the most strongly associated with WBSF in Limousin ($-\log_{10}P = 3.23$). However, *rs42192103* was found to be slightly more strongly associated with WBSF than *rs17812000* in the across-breed analysis ($-\log_{10}P = 15.25$ vs. 15.01), with an average ASE across breeds of 0.23 kg (Table S3). The amount of phenotypic variation explained in the haplotype-based analyses again indicates that none of the tested SNPs are causal for effects on WBSF and that the strongest signal for association with WBSF was in the 8187-bp region from 44 062 694 to 44 070 881 in all five breeds (Table S3). The size of this region is sufficiently small to speculate that there is probably only a single mutation in *CAPN1* affecting WBSF in all *Bos t. taurus* cattle breeds, and the across-breed haplotype analysis shown in Table S3 and Fig. 2 suggests that the most

Table 3 Percentages of phenotypic variation in WBSF explained by the commercialized SNPs, the most strongly associated SNPs and haplotypes within the most strongly associated nine SNP window within *CAST* and *CAPN1*.

Locus	All breeds	Angus	Hereford	Charolais	Limousin	Simmental
<i>CAST</i> (BTA7)						
<i>rs41255587</i> ¹	0.66	0.53	1.47	1.14	0.70	0.02
98 579 574						
SNP ²	0.66	0.54	1.47	1.14	2.28	1.13
98 579 574		98 498 047	98 579 574	98 579 574	97 861 341	98 013 150
Window-P ³	1.02	1.36	1.88	2.10	3.88	2.77
98 495 888		98 495 888	98 566 391	98 538 952	97 501 859	97 861 341
Window-V _P ⁴	1.02	1.36	1.92	2.10	4.02	2.77
98 495 888		98 495 888	98 495 888	98 538 952	98 375 640	97 861 341
<i>CAPN1</i> (BTA29)						
<i>rs17812000</i> ¹	1.14	2.36	0.96	1.38	0.00	3.75
44 069 063						
<i>rs17871051</i> ¹	0.39	1.54	0.16	0.39	0.57	1.66
44 085 642						
<i>rs17872050</i> ¹	0.53	0.89	0.08	1.21	2.88	1.65
44 097 629						
SNP ²	1.16	2.36	1.62	1.57	2.88	4.65
44 070 713		44 069 063	44 067 796	44 070 713	44 087 629	44 042 363
Window-P ³	1.80	3.18	2.59	2.76	2.99	5.05
44 067 796		44 068 519	44 062 694	44 070 881	44 087 356	44 067 234
Window-V _P ⁴	1.85	3.19	2.59	2.76	3.52	5.35
44 068 143		44 068 445	44 062 694	44 070 881	44 070 881	44 068 143

CAST, calpastatin; *CAPN1*, calpain 1, (*mu*/I) large subunit; SNP, single-nucleotide polymorphism; WBSF, Warner–Bratzler shear force.

¹Commercialized SNP and its chromosomal coordinate.

²Most strongly associated SNP and its chromosomal coordinate.

³Most strongly associated nine SNP window centred on SNP with shown chromosomal coordinate.

⁴Nine SNP window explaining the greatest amount of phenotypic variation in WBSF.

likely region harbouring this mutation is the 4581-bp region from 44 063 938 to 44 068 519. This region is wholly contained within the 5' end of *CAPN1*. We estimate from the haplotype analysis that *CAPN1* explains 1.85% of the phenotypic variation in WBSF in taurine cattle (Table 3).

Conclusions

We conclusively demonstrate that none of the SNPs currently commercialized as diagnostics for genetic merit are causal for their effects on WBSF (Casas *et al.* 2003, 2006; Van Eenennaam *et al.* 2007; Gill *et al.* 2009). In fact, the complex patterns of LD in the vicinity of these genes among the different breeds (Figs S2 and S3) and the weaker associations in Limousin and Simmental (Fig. S1) result in different SNPs being most strongly associated with WBSF among the breeds (Table S3). However, by using haplotype-based analysis methods to dissect the variation within these genes, we localized the causal variants to be 5' to the commercially tested SNPs. In the case of *CAPN1*, the higher SNP density achieved and the use of across-breed analysis, which erodes the patterns of LD within breeds, resolved the likely location of the causal variant to a region of only 4581 bp.

We found evidence for a large number of QTL underlying variation in WBSF, and the majority of the previously published QTL were validated in this analysis. We found reasonably strong evidence that most QTL were segregating in all five breeds; however, the small genetic sample sizes for Limousin and Simmental make this comparison problematic, and it remains an unanswered question as to the extent to which breeds may share private alleles at QTL. This has previously been found in Belgian Blue, Marchigiana and Piedmontese cattle, where breed-specific polymorphisms in *MSTN* produce the double muscled phenotype (Grobet *et al.* 1997; Kambadur *et al.* 1997; McPherron & Lee 1997; Marchitelli *et al.* 2003). This issue is of importance to the development of prediction equations for molecular breeding values in across-breed analyses, because the ASEs estimated for QTL regions will be averaged across breeds that segregate and those that do not segregate for certain QTL, which will limit the accuracy of molecular estimates of breeding value. Despite this, we found moderate correlations between GBLUP predictions of ASEs computed in the across- and within-breed analyses, suggesting that the BovineSNP50 assay has sufficient resolution for the development of prediction equations for genomic selection in beef cattle despite their considerably larger effective population size relative to

dairy cattle (The Bovine HapMap Consortium 2009), and also that WBSF QTL are commonly shared among breeds.

Despite the apparent reduced complexity of a trait such as meat tenderness relative to growth, there appear to be a large number of QTL underlying variation in WBSF, and the identification of all of the mutations that underlie these QTL might appear to be intractable. However, recent developments in high-density SNP genotyping, high-throughput sequencing and genotype imputation suggest new strategies for the rapid simultaneous identification of variants underlying quantitative traits genome-wide. We accomplished an average SNP spacing of 1139 bp for the 23 SNPs analysed within *CAPN1*, and this is only slightly smaller than could be accomplished genome-wide by jointly genotyping with the newly available Illumina BovineHD and Affymetrix BOS 1 assays (~1.3 million SNP, data not shown). Furthermore, the design of these assays was facilitated by a community effort that produced more than 128.4X of genome sequence coverage on more than 80 animals, and SNP data from this work are now available in dbSNP. This project discovered 48.6 million high-quality SNPs, which must include many of the causal variants underlying quantitative variation in cattle, and it may be possible to impute genotypes at the resolution of the genome sequence (Daetwyler *et al.* 2011) in populations that have been genotyped with both assays. Such a strategy could rapidly allow the identification of a large number of causal variants if the association analysis was performed in mixed breed populations.

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Supporting information

Additional supporting information may be found in the online version of this article.

Figure S1 Manhattan plots of normalized single-nucleotide polymorphism allele substitution effects for each breed.

Figure S2 Linkage disequilibrium (LD) plots (r^2) created in HAPLOVIEW v4.1 for 44 single-nucleotide polymorphisms spanning 2.86 Mb centred on *calpastatin* on BTA7.

Figure S3 Linkage disequilibrium (LD) plots (r^2) created in HAPLOVIEW v4.1 for the 100 single-nucleotide polymorphisms spanning 3.12 Mb centred on *CAPN1* on BTA29.

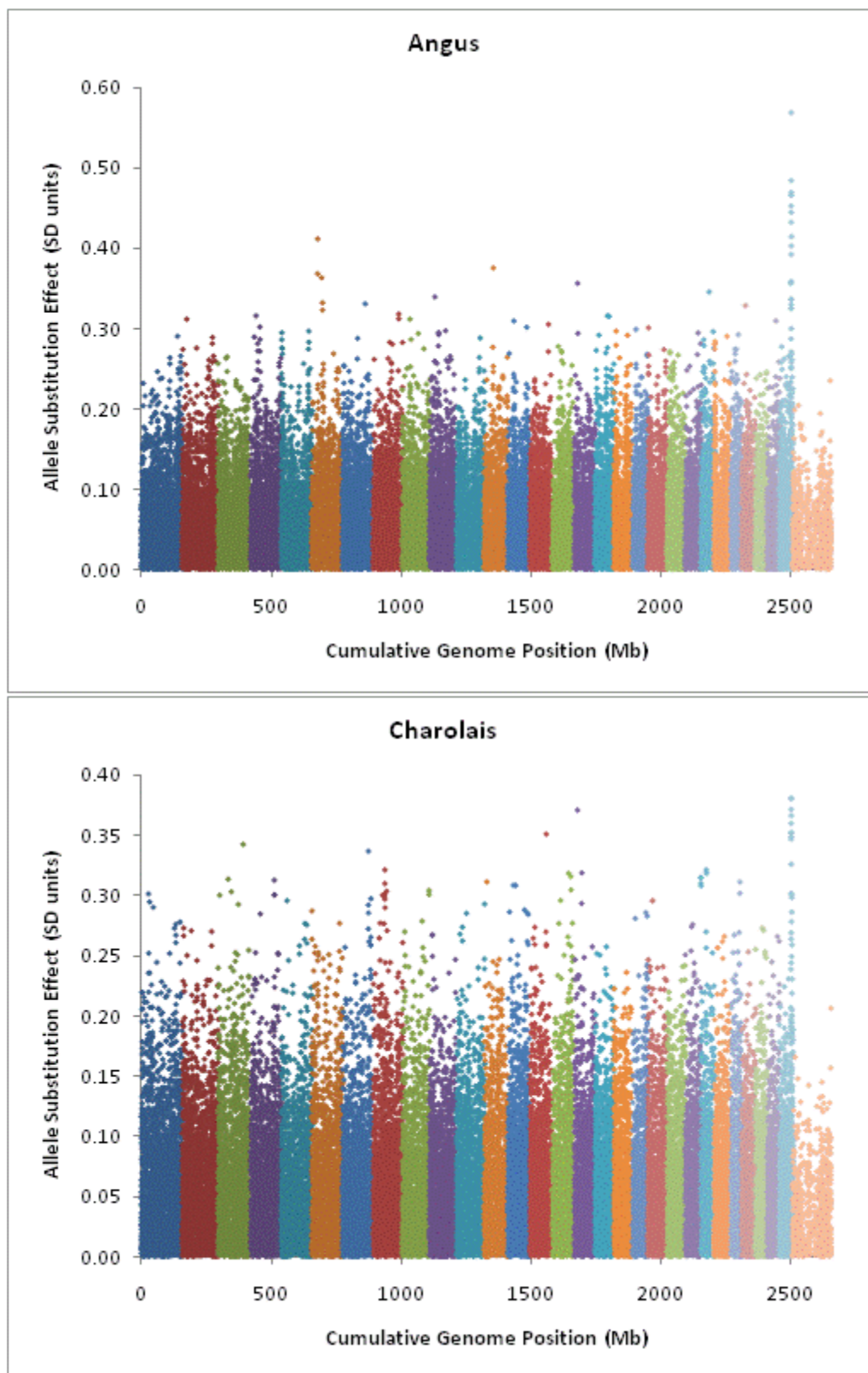
Table S1 Characteristics of single-nucleotide polymorphisms located near *calpastatin* and *calpain 1*, (*mu/I*) large subunit that were designed into the Illumina GoldenGate assay and genotyped in 3240 CMP animals.

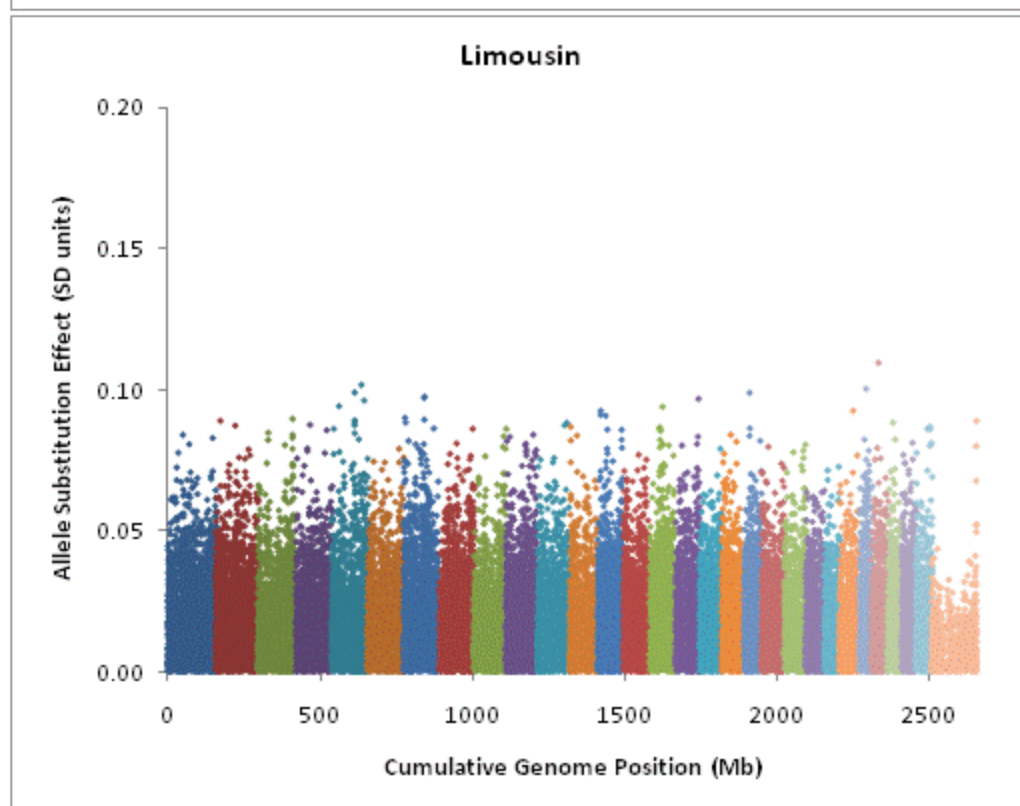
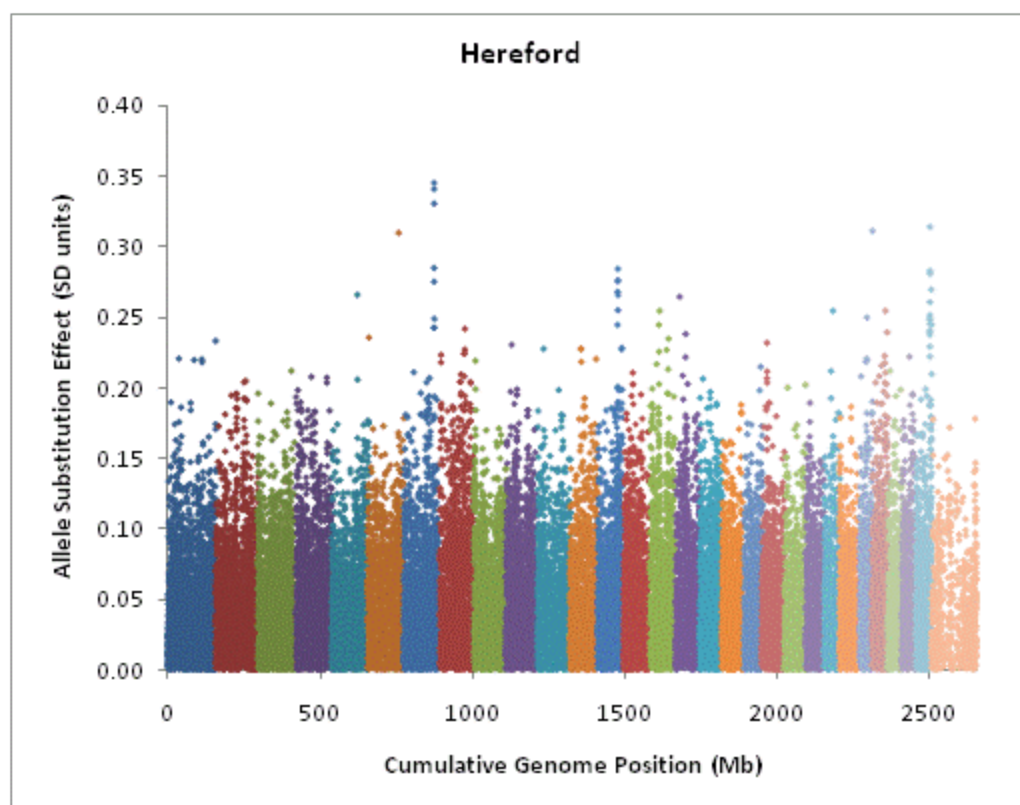
Table S2 Standardized single-nucleotide polymorphism allele substitution effects, within-breed *t*-like statistic ranks, heterozygosity, allele frequency and sliding window rank information.

Table S3 Patterns of single-nucleotide polymorphism association with Warner–Bratzler shear force for *calpastatin* and *calpain 1*, (*mu/I*) large subunit loci.

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Figure S1. Manhattan plots of normalized SNP allele substitution effects for each breed.





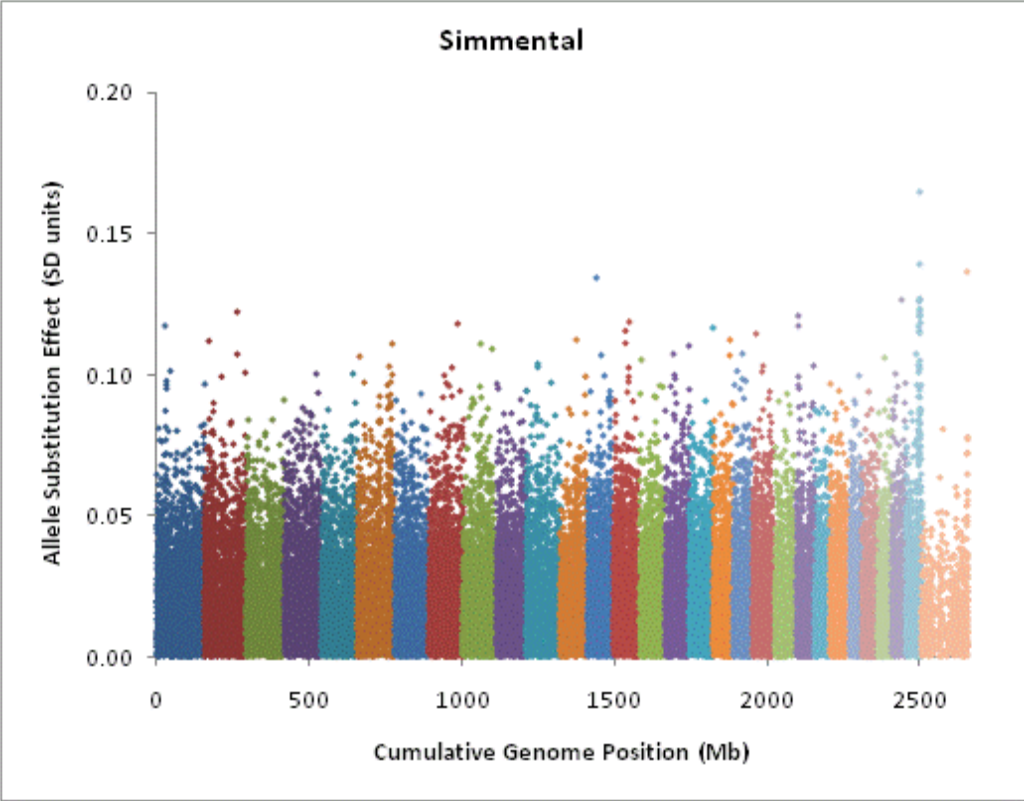
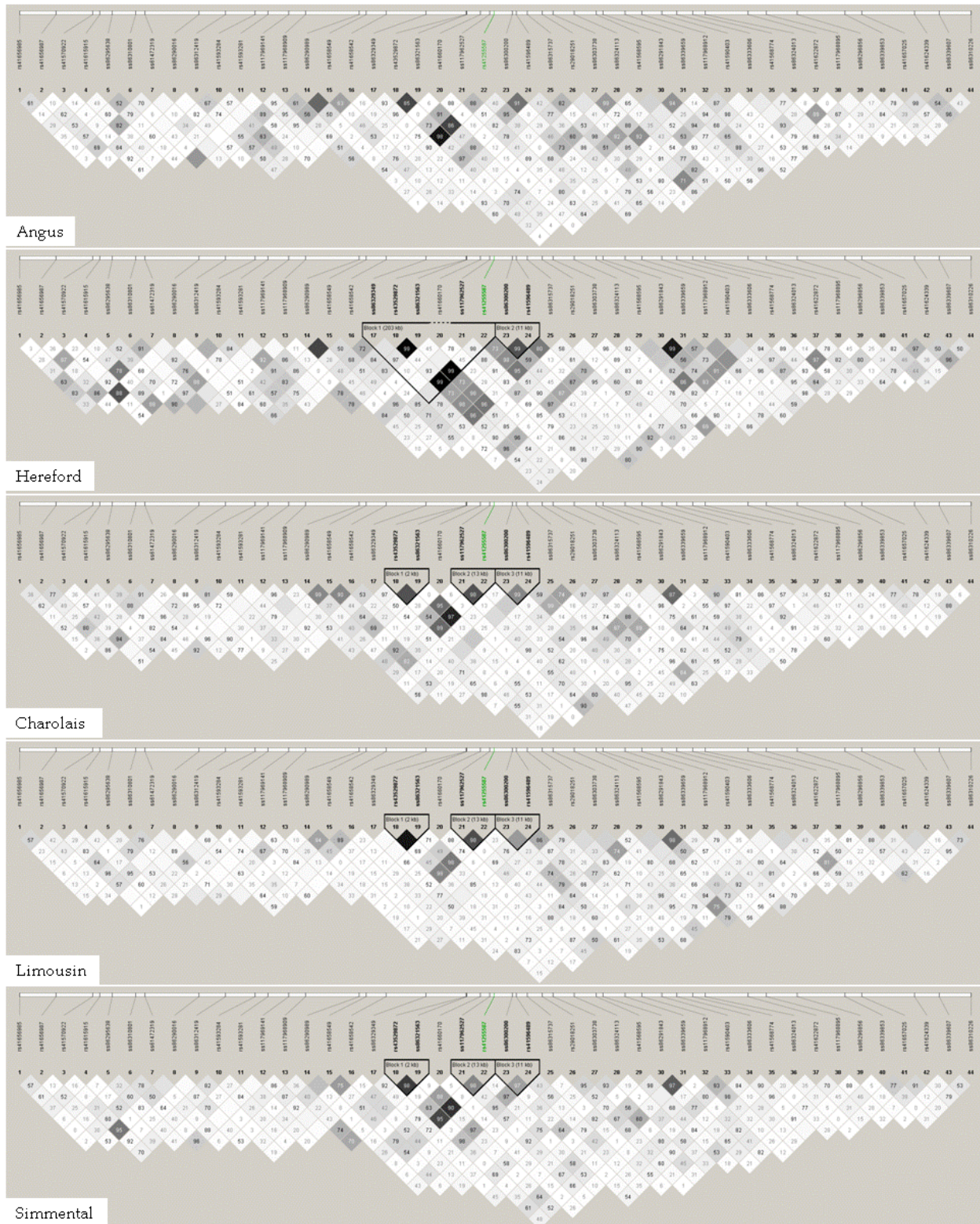


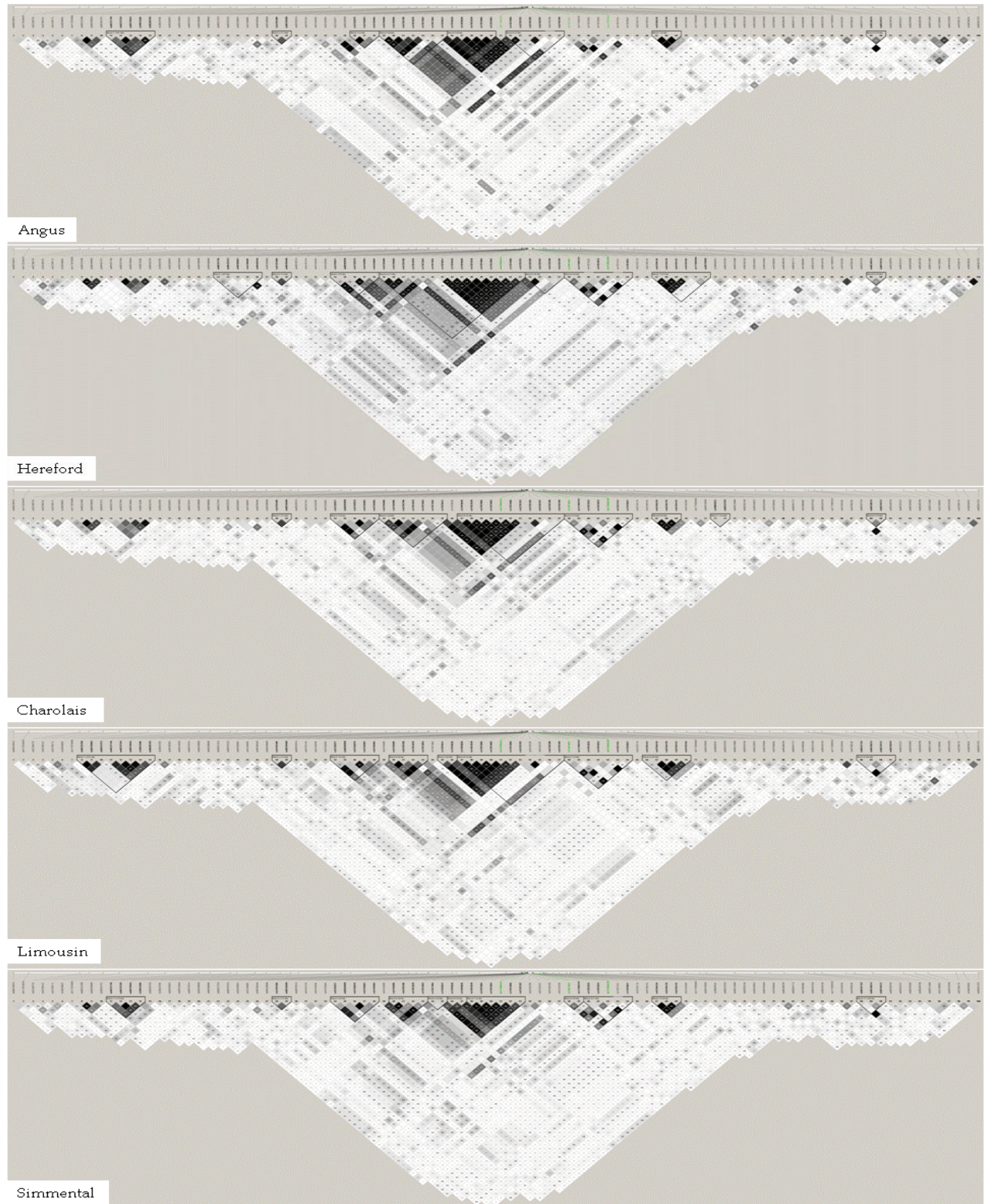
Figure S2 Linkage disequilibrium (LD) plots (r^2) created in Haploview v4.1 (Barrett *et al.* 2005) for 44 SNP spanning 2.86 Mb centered on *CAST* on BTA7. Darker shading indicates regions of higher LD. The commercially tested SNP, *rs41255587*, (#22) is highlighted in green.



References

Barrett J.C., Fry B., Maller J. & Daly M.J. (2005) Haploview: analysis and visualization of LD and haplotype maps. *Bioinformatics* **21**, 263-5.

Figure S3 Linkage disequilibrium (LD) plots (r^2) created in Haploview v4.1 (Barrett *et al.* 2005) for the 100 SNP spanning 3.12 Mb centered on *CAPN1* on BTA29. Darker shading indicates regions of higher LD. The commercially tested SNP, *rs17812000* (#51), *rs17871051* (#58), and *rs17872050* (#62) are highlighted in green.



References

Barrett J.C., Fry B., Maller J. & Daly M.J. (2005) Haploview: analysis and visualization of LD and haplotype maps. *Bioinformatics* **21**, 263-5.

Table S1 Characteristics of SNPs located near *CAST* and *CAPN1* that were designed into the Illumina GoldenGate assay and genotyped in 3,240 CMP animals

SNP ID ¹	BTA	POS ²	Filtered ³	Call Rate (%)					A Allele Frequency				
				Angus	Hereford	Charolais	Limousin	Simmental	Angus	Hereford	Charolais	Limousin	Simmental
<i>rs42269174</i>	7	98,260,103	AF	99.09	98.41	99.00	89.47	97.89	0.0000	0.0009	0.0000	0.0000	0.0000
<i>rs42269169</i>	7	98,346,128	AF	99.09	97.82	99.00	89.12	97.50	1.0000	0.9991	1.0000	0.9980	0.9990
<i>rs42269168</i>	7	98,351,749	CR,AF	93.48	92.03	96.58	88.42	95.20	0.9749	0.9699	0.9904	0.9782	0.9808
<i>rs42269166</i>	7	98,381,155	AF	98.79	97.57	99.00	90.18	97.89	0.0000	0.0000	0.0000	0.0039	0.0000
<i>rs42269167</i>	7	98,406,957	AF	98.64	96.90	99.15	91.23	98.46	0.0077	0.0074	0.0101	0.0058	0.0058
<i>rs42269164</i>	7	98,414,333	CR,AF	98.94	96.81	97.72	88.42	96.93	0.9985	0.9931	0.9942	0.9940	0.9851
<i>rs42269165</i>	7	98,423,052	CR,AF	98.94	97.57	98.72	88.77	97.70	0.0000	0.0000	0.0000	0.0000	0.0000
<i>rs43529864</i>	7	98,446,203	AF	98.94	97.57	98.86	89.82	97.89	0.0000	0.0000	0.0000	0.0000	0.0000
<i>rs43529865</i>	7	98,447,598	AF	98.64	97.06	99.00	89.12	97.31	1.0000	1.0000	1.0000	1.0000	1.0000
<i>rs43529866</i>	7	98,450,896	AF	99.24	98.57	99.15	89.82	97.89	1.0000	0.9991	1.0000	1.0000	1.0000
<i>rs43529867</i>	7	98,462,790	AF	99.09	98.07	98.86	90.18	98.27	0.0000	0.0000	0.0000	0.0000	0.0010
<i>rs43529868</i>	7	98,465,338	AF	98.94	97.48	98.29	89.12	97.89	1.0000	0.9991	1.0000	1.0000	0.9980
<i>rs41596484</i>	7	98,481,587	AF	99.09	97.90	98.86	89.82	97.50	0.0122	0.0043	0.0677	0.0137	0.0600
<i>rs41596488</i>	7	98,482,088	CR	99.09	97.32	98.43	88.77	97.31	0.7768	0.4767	0.7359	0.8241	0.5592
<i>rs43529869</i>	7	98,486,784	AF	98.18	97.06	98.72	90.18	97.12	0.0000	0.0000	0.0000	0.0000	0.0000
<i>rs43529872</i>	7	98,495,888		99.09	98.15	98.72	90.18	98.08	0.2064	0.5094	0.1912	0.1518	0.3630
<i>rs43529870</i>	7	98,503,071	CR,AF	95.15	77.10	93.02	89.82	84.84	0.9968	0.9717	0.9931	0.9961	0.9706
<i>rs41619071</i>	7	98,601,495	DNC										
<i>rs43529862</i>	7	98,525,723	AF	99.24	98.24	98.58	89.82	97.70	0.9992	0.9983	0.9993	1.0000	0.9951
<i>rs41660170</i>	7	98,538,952		99.09	97.06	99.15	90.18	98.08	0.0749	0.0402	0.1121	0.0856	0.0646
<i>rs42776088</i>	7	98,559,498	AF	99.09	95.72	98.86	89.82	97.50	1.0000	0.9982	1.0000	1.0000	0.9990
<i>rs42776087</i>	7	98,574,830	CR	98.94	96.73	98.29	88.77	96.35	0.2213	0.5108	0.2471	0.2688	0.4373
<i>rs41255587</i>	7	98,579,574		98.64	96.31	98.01	89.47	96.55	0.2166	0.5109	0.2406	0.2725	0.4205
<i>rs42776090</i>	7	98,620,447	AF	99.24	98.49	99.00	89.82	98.08	1.0000	0.9991	1.0000	0.9980	0.9980
<i>rs41596489</i>	7	98,646,770		99.24	98.15	98.72	89.12	97.70	0.4901	0.6970	0.6154	0.7756	0.6916
<i>rs43529875</i>	7	98,680,392	AF	99.09	98.07	98.58	89.12	98.46	1.0000	0.9987	1.0000	1.0000	0.9951
<i>rs43529877</i>	7	98,701,638	AF	99.24	98.57	99.15	89.82	98.27	0.0023	0.0060	0.0036	0.0059	0.0020
<i>rs41657006</i>	7	98,709,304	CR	93.94	78.69	85.33	85.61	55.09	0.3750	0.2655	0.3038	0.2111	0.2648
<i>rs43101783</i>	29	43,924,518	AF	98.79	97.65	97.72	89.47	96.93	0.9969	0.9987	0.9942	0.9902	0.9990
<i>rs42191319</i>	29	44,000,728		98.64	96.81	98.72	90.88	97.50	0.0630	0.2959	0.0938	0.0946	0.1358

rs42192038	29	44,029,526		98.33	97.99	98.58	89.47	97.31	0.4923	0.5801	0.3736	0.2137	0.3481
rs42192064	29	44,042,363		99.09	98.15	99.00	89.47	98.27	0.6284	0.4526	0.4187	0.3902	0.4014
rs42192074	29	44,047,246	CR	98.18	96.73	97.44	88.77	95.59	0.6420	0.6019	0.6235	0.5929	0.6235
rs42192077	29	44,049,244		98.64	97.48	98.29	89.12	97.50	0.3510	0.3972	0.3652	0.3878	0.3376
rs42192079	29	44,051,567		98.33	96.56	98.15	89.82	97.31	0.6456	0.6012	0.6277	0.5938	0.6282
rs42192083	29	44,053,733		99.24	97.57	97.72	90.18	96.93	0.3573	0.4015	0.3754	0.4027	0.3663
rs42192084	29	44,054,901		98.94	96.90	98.15	89.12	95.20	0.7940	0.7290	0.7736	0.7539	0.8115
rs41596485	29	44,054,902	CR	9.09	5.03	8.55	12.98	4.99	0.5000	0.4917	0.5000	0.4865	0.5000
rs42192090	29	44,058,688		98.79	98.15	99.00	89.47	98.08	0.4410	0.5679	0.4626	0.6412	0.4374
rs42192096	29	44,060,410		99.24	97.82	98.86	90.18	98.08	0.5534	0.4125	0.4697	0.2899	0.5548
rs42192100	29	44,062,694		98.79	97.23	98.01	89.82	96.74	0.5529	0.4142	0.4731	0.2910	0.5595
rs17872077	29	44,063,844	CR	87.12	84.90	91.03	79.30	85.99	0.1122	0.1260	0.0845	0.0664	0.0993
rs41657009	29	44,063,937	DNC						0.0000	0.0000	0.0000	0.0000	0.0000
rs17872078	29	44,063,938		98.94	96.98	98.72	90.18	97.70	0.4893	0.2171	0.3333	0.1868	0.3536
rs17872101	29	44,066,634	AF	99.09	98.49	99.00	90.18	98.46	0.0000	0.0000	0.0000	0.0000	0.0000
rs17871028	29	44,067,079	AF	99.24	96.98	98.86	89.82	97.31	0.0031	0.0078	0.0029	0.0000	0.0286
rs17872081	29	44,067,161	AF	98.48	97.90	98.43	89.82	97.89	0.0000	0.0004	0.0000	0.0000	0.0020
rs17872093	29	44,067,234		99.24	97.48	97.72	89.82	97.31	0.4466	0.5856	0.5313	0.7090	0.4438
rs17872094	29	44,067,596	CR	62.27	56.71	73.36	49.47	69.10	0.3917	0.6198	0.5427	0.4681	0.6153
rs17871984	29	44,067,796		99.24	97.65	98.58	90.18	98.46	0.1260	0.2302	0.2406	0.1498	0.3343
rs17870633	29	44,067,919	AF	98.94	98.07	98.86	90.18	97.31	0.0000	0.0004	0.0007	0.0000	0.0020
rs17871987	29	44,067,984	CR	99.24	97.73	98.72	88.77	97.50	0.4267	0.1833	0.2302	0.1403	0.2185
rs17870631	29	44,068,143		99.24	97.99	98.72	90.53	98.08	0.5725	0.8134	0.7691	0.8566	0.7789
rs17870630	29	44,068,247	AF	99.24	98.24	98.58	90.18	97.89	1.0000	0.9996	1.0000	1.0000	1.0000
rs17870628	29	44,068,346		98.94	97.48	98.01	89.47	97.89	0.5352	0.8081	0.7071	0.7902	0.7010
rs17870626	29	44,068,445		99.09	97.82	98.72	90.18	96.55	0.5680	0.8135	0.7655	0.8521	0.7465
rs17872010	29	44,068,519		98.94	97.23	97.72	90.18	97.31	0.5743	0.8162	0.7682	0.8560	0.7761
rs17872004	29	44,068,580		98.33	97.40	98.29	90.18	95.97	0.5732	0.8178	0.7703	0.8541	0.7820
rs17872003	29	44,068,812		97.58	96.39	98.15	89.82	96.93	0.4278	0.1819	0.2315	0.1445	0.2188
rs17872000	29	44,069,063		98.18	95.72	99.43	99.30	99.23					
rs17872006	29	44,069,177		96.21	97.23	97.86	89.47	97.12	0.4299	0.1877	0.2394	0.1451	0.2322
rs42192102	29	44,070,590	CR	98.79	97.23	98.15	87.72	97.70	0.4371	0.5669	0.5203	0.6860	0.3978
rs42192103	29	44,070,713		96.67	95.81	98.29	89.82	96.55	0.4326	0.1988	0.2355	0.1641	0.2674
rs42192105	29	44,070,881		98.79	97.57	97.72	89.47	97.31	0.1304	0.1561	0.0707	0.0431	0.0966

rs42192107	29	44,071,034		98.94	97.48	98.72	90.53	97.70		0.1187	0.1506	0.0592	0.0426	0.0452
rs42192108	29	44,071,135		99.09	97.32	98.43	89.82	97.70		0.0344	0.1858	0.1606	0.0781	0.0472
rs42192109	29	44,071,593		98.79	96.90	98.58	89.47	97.31		0.4954	0.3935	0.3728	0.2667	0.4043
rs42192110	29	44,071,657	CR	99.24	97.65	98.15	88.42	97.89		0.5595	0.4214	0.4768	0.3056	0.5500
rs42192111	29	44,071,828	CR,AF	74.24	63.17	60.97	44.91	63.34		1.0000	0.9967	1.0000	0.9844	0.9970
rs42192117	29	44,081,264	AF	98.18	97.23	98.86	89.82	97.50		0.0000	0.0000	0.0000	0.0000	0.0010
rs17870499	29	44,085,195	CR	98.64	97.40	98.58	88.07	97.70		0.0499	0.0263	0.0874	0.1096	0.0697
rs17871051	29	44,085,642		99.39	97.65	98.29	89.12	97.50		0.0998	0.1044	0.3659	0.3996	0.3051
rs17871058	29	44,085,769	DNC*											
rs17871060	29	44,086,042	AF	99.24	98.07	98.29	89.82	96.55		1.0000	1.0000	1.0000	0.9961	1.0000
rs17872027	29	44,086,761	AF	99.24	97.82	99.00	90.53	97.89		0.0061	0.1677	0.0259	0.0174	0.0216
rs17872030	29	44,086,943	CR	98.64	97.40	98.29	88.42	96.35		0.0975	0.1047	0.3616	0.4028	0.3058
rs17872031	29	44,087,019	AF	94.70	97.82	96.58	90.53	98.27		0.0160	0.0262	0.0133	0.0000	0.0078
rs17872032	29	44,087,205		98.33	97.32	98.15	90.18	96.93		0.0493	0.0250	0.0842	0.0953	0.0683
rs17872033	29	44,087,356		97.58	96.31	97.58	89.82	95.39		0.8960	0.8916	0.6263	0.5938	0.6620
rs17872050	29	44,087,629		99.55	96.64	99.29	99.65	99.04						
rs17872151	29	44,087,858		99.09	97.90	98.15	90.18	97.70		0.0153	0.0167	0.0856	0.1323	0.0452
rs17872153	29	44,088,027	CR	99.09	97.65	98.01	87.72	96.93		0.9893	0.9854	0.8990	0.8360	0.9010
rs17870855	29	44,088,451	CR	98.79	97.15	98.43	88.77	96.93		0.0997	0.1036	0.3647	0.4071	0.3267
rs17870847	29	44,088,897		99.24	97.23	98.72	90.53	98.08		0.7038	0.8352	0.4531	0.3217	0.5284
rs17870848	29	44,089,043	CR	88.94	91.78	91.31	81.05	91.55		0.6457	0.5457	0.6131	0.5714	0.5461
rs42192119	29	44,110,295		99.24	98.24	98.86	89.82	98.08		0.3267	0.4539	0.4150	0.4219	0.3591
rs42192125	29	44,112,272	AF	99.09	97.73	99.15	90.88	98.46		0.0000	0.0000	0.0000	0.0019	0.0010
rs42195143	29	44,119,671		96.82	96.31	98.29	90.18	96.35		0.5939	0.6224	0.6203	0.5233	0.6365
rs42194216	29	44,122,272		99.09	98.07	98.86	89.82	97.70		0.0956	0.1737	0.0620	0.1543	0.1130
rs42194178	29	44,125,747		99.55	98.07	98.86	90.88	97.89		0.0951	0.1698	0.0641	0.1544	0.1118
rs42194132	29	44,130,887		99.09	97.15	99.15	89.12	97.70		0.9060	0.8286	0.9368	0.8465	0.8870
rs42193349	29	44,154,126		98.18	97.32	98.01	89.12	97.50		0.0332	0.1586	0.0334	0.1240	0.0827
rs42193335	29	44,163,955	AF	99.09	97.99	98.72	89.82	97.31		1.0000	0.9991	1.0000	0.9961	1.0000
rs41586223	29	44,196,154	DNC											
rs29003633	29	44,208,978		98.94	97.99	99.00	90.18	97.89		0.0398	0.0424	0.0540	0.0136	0.0480
rs42195220	29	44,235,914	AF	99.24	98.49	99.15	90.53	98.27		0.0000	0.0000	0.0000	0.0000	0.0000
¹ Identities of commercialized SNPs predictive of tenderness are shaded in red. Identities of SNPs within <i>CAST</i> and <i>CAPN1</i> are shaded in yellow.														
Bold SNPs have been removed from dbSNP.														

² Base pair position from the UMD3.1 sequence assembly.								
³ Reason for filtering SNP from analysis. DNC=Did not convert, AF=Allele Frequency, CR=Call rate. * = Also included on BovineSNP50 assay.								

Table S3. Patterns of SNP association with WBSF for CAST and CAPN1 loci.								
					Rank ³			
BTA	POS ¹	SNP ID ²	All Breeds	Angus	Hereford	Charolais	Limousin	Simmental
7	97,151,592	rs41656985	17853	22832	22123	11997	40460	19009
7	97,261,052	rs41656987	654	5620	39476	13999	1891	2069
7	97,372,656	rs41570922	20417	16753	26124	38433	14071	33362
7	97,393,157	rs41615915	1427	37659	39656	1009	17193	6660
7	97,430,691	ss86295638	3045	39136	27527	1047	23654	13621
7	97,501,859	ss86310801	13413	33096	22602	19582	10997	16395
7	97,529,872	ss61472319	10706	16140	20625	1743	6464	29536
7	97,691,853	ss86290016	30824	31090	22986	36148	36108	24197
7	97,772,240	ss86312419	10263	8991	28755	7170	16285	37994
7	97,861,341	rs41593284	921	27589	4833	32544	37	17064
7	97,898,940	rs41593281	50	10852	33	23180	32882	6820
7	97,961,659	ss117969141	28454	25196	38529	39653	37599	25297
7	98,013,150	ss117968909	35590	29216	1170	4574	26692	308
7	98,173,299	ss86290989	30594	29793	9717	4845	29926	29007
7	98,194,828	rs41658549	34336	6424	2534	90	30247	15824
7	98,254,815	rs41658542	13991	24584	267	603	11619	21439
7	98,375,640	ss86329349	1790	4605	1593	38596	23512	33940
7	98,495,888	rs43529872	13	610	3	57	3069	20634
7	98,498,047	ss86321563	12	294	2	66	6102	15068
7	98,538,952	rs41660170	8319	6163	39936	10548	29756	20353
7	98,566,391	ss117962527	1310	2288	27900	619	20424	39851
7	98,579,574	rs41255587	10	237	1	14	2479	27896
7	98,635,208	ss86300200	37	11749	7	11342	4871	8383
7	98,646,770	rs41596489	34	628	11	38675	17319	30575
7	98,680,293	ss86315737	250	465	34	18680	14562	39284
7	98,726,055	rs29018251	13126	848	5956	5486	38597	28483
7	98,757,265	ss86303738	17394	26602	27914	20844	34152	5174
7	98,820,742	ss86324113	137	746	150	29169	22220	2224
7	98,887,313	rs41568595	15241	35496	29107	8018	38017	32238
7	98,907,404	ss86291843	9022	39450	9020	20771	4773	22927
7	98,974,456	ss86339659	7758	16220	6313	25941	24786	34105
7	99,024,444	ss117968912	24262	20693	6213	1798	15823	13240
7	99,085,299	rs41590403	9428	20682	24941	9134	4854	30656
7	99,130,598	ss86333606	1878	35186	26	34124	33105	11400
7	99,178,748	rs41568774	33934	35119	17840	37290	16533	18785
7	99,215,474	ss86324013	5728	38209	1565	37408	34561	25708
7	99,344,820	rs41622872	1488	20805	292	22465	1993	7618
7	99,399,852	ss117968895	37103	18064	39777	21174	35095	37490
7	99,492,904	ss86296856	6124	5452	40099	5651	36078	36085
7	99,635,841	ss86339853	32326	35802	7339	10001	11279	8481
7	99,687,614	rs41657025	19734	6764	15594	21139	38911	6044
7	99,845,133	rs41624339	1593	28933	13874	1849	16503	9618
7	99,919,908	ss86339607	35826	32733	12431	40446	13228	18950
7	100,015,468	ss86310226	27936	27227	9309	36010	12692	15892
29	42,406,544	ss86319674	37050	4925	23582	28260	21027	18936
29	42,455,680	ss117974470	22297	37162	29770	25573	5930	7326
29	42,620,218	rs42189770	35226	28646	8272	20924	33490	30054
29	42,651,294	rs43706142	28368	1526	13688	20292	33318	33867
29	42,696,595	rs42189112	11135	4128	567	12339	38243	4930
29	42,749,808	rs29020063	28224	13151	2449	29252	12285	1538
29	42,842,353	ss117974486	8500	5777	7774	25144	6122	24
29	42,897,144	ss86322358	27082	14890	31939	27607	33377	7184

29	43,006,000	ss86339964	32865	10952	32290	27608	33378	10290
29	43,043,207	ss86341572	20145	5329	32350	4763	12546	3676
29	43,108,445	ss86337140	608	1800	3230	19455	27355	8204
29	43,129,250	ss86337549	7614	933	38609	37467	9721	22158
29	43,189,370	ss86319044	9896	929	38610	39410	15557	22159
29	43,224,753	rs29013208	9469	1268	37486	27816	15836	8935
29	43,269,744	ss86282762	16588	2397	36965	25543	21052	24438
29	43,304,256	rs29024708	5161	1726	19477	22317	32243	344
29	43,328,607	ss86295061	35423	2869	9694	11234	25778	26570
29	43,429,511	ss86318094	42	66	37	20269	10690	7322
29	43,466,342	ss86310741	7210	889	20819	12113	6737	11755
29	43,498,073	ss86338800	1179	1059	26456	1057	12237	4447
29	43,611,640	ss86298040	77	13108	2175	227	27133	175
29	43,652,252	ss86327310	309	28	6692	33574	14789	1316
29	43,686,401	ss86325323	30559	1290	10319	11271	38311	16973
29	43,709,769	ss86290081	6403	191	4662	9805	15489	17693
29	43,747,765	rs42190085	9036	19561	38491	8579	26434	27476
29	43,749,527	ss86299346	25366	23606	37713	17640	33965	21036
29	43,777,249	ss86299989	35438	2116	35762	18707	39614	29763
29	43,826,144	rs42191289	31815	3320	9684	22649	7809	192
29	43,839,783	ss86336460	5396	729	9980	6073	17672	49
29	43,914,923	ss86335514	24	6410	3157	114	8553	102
29	44,000,728	rs42191319	22471	40614	11851	25045	22311	31987
29	44,029,526	rs42192038	1251	6182	24398	4384	19663	609
29	44,042,363	rs42192064	21	182	3321	11547	31563	1
29	44,049,244	rs42192077	8485	17117	1831	29917	40623	33046
29	44,050,471	ss86284058	3336	26458	559	8623	33356	13451
29	44,051,567	rs42192079	11270	22597	2795	29554	39615	31917
29	44,053,733	rs42192083	12323	17992	2555	32354	36798	30606
29	44,054,901	rs42192084	22522	24469	12212	13490	30189	18346
29	44,058,688	rs42192090	6685	2065	17751	201	10644	9852
29	44,060,410	rs42192096	7985	1898	10671	887	17953	3893
29	44,062,694	rs42192100	8555	1844	10835	1333	20163	4552
29	44,063,938	rs17872078	8	12	36	15	29894	25
29	44,067,234	rs17872093	10292	1899	6796	888	20164	3580
29	44,067,796	rs17871984	11	44	4	2066	19038	516
29	44,068,143	rs17870631	2	4	24	7	39018	6
29	44,068,346	rs17870628	14	16	19	750	22524	269
29	44,068,445	rs17870626	6	7	29	12	31903	5
29	44,068,519	rs17872010	7	6	40	8	39019	13
29	44,068,580	rs17872004	4	5	27	11	36321	9
29	44,068,812	rs17872003	5	3	28	6	35508	12
29	44,069,063	rs17812000	3	1	59	9	39020	10
29	44,069,177	rs17872006	9	2	46	40	24824	14
29	44,070,713	rs42192103	1	8	9	1	25633	2
29	44,070,881	rs42192105	394	6164	200	30967	37715	10226
29	44,071,034	rs42192107	495	5948	183	22528	37716	21810
29	44,071,135	rs42192108	10891	35181	23330	21578	9516	38169
29	44,071,593	rs42192109	1089	193	26124	100	11867	2864
29	44,085,642	rs17871051	22	22	8993	829	3823	128
29	44,085,769	rs17871058	16	29	10865	5	82	44
29	44,087,205	rs17872032	977	3035	36234	2335	14676	3236
29	44,087,356	rs17872033	27	26	9090	1020	2073	337
29	44,087,629	rs17872050	15	17	11193	3	30	54
29	44,087,858	rs17872151	7794	38670	21318	12661	22722	19232

29	44,088,897	rs17870847	17	23	13127	2	39	91
29	44,110,295	rs42192119	24761	30393	34998	11139	17791	29587
29	44,119,671	rs42195143	27184	13786	2181	33844	29050	24476
29	44,122,272	rs42194216	17667	28444	8083	27006	31593	40203
29	44,125,747	rs42194178	16874	25410	6562	27074	31594	40204
29	44,130,887	rs42194132	20944	25411	7613	26871	31592	31199
29	44,154,126	rs42193349	13422	10208	5641	31876	28607	21748
29	44,172,614	ss117965984	3742	39565	4851	10280	24312	5842
29	44,196,154	ss86318958	29029	13994	8832	22414	34749	33087
29	44,208,978	rs29003633	19817	1795	39702	33937	39148	28356
29	44,223,148	ss86323783	1050	105	36704	940	9476	28615
29	44,243,444	ss86313099	32174	543	399	4467	31547	19210
29	44,325,408	ss86292140	41	11	14276	2309	15992	648
29	44,372,611	ss86329852	15417	38369	20426	2699	9819	8295
29	44,395,075	ss86333994	275	979	2714	33693	22902	210
29	44,416,282	rs43709648	18	149	10	1683	32992	14042
29	44,546,564	ss86288185	494	1548	1310	4321	35230	12565
29	44,585,782	ss86341172	2967	2916	9784	1728	16607	18099
29	44,628,137	rs41600300	35992	11176	30882	26481	13878	19086
29	44,649,908	ss86337530	36291	30728	2567	18016	29243	4361
29	44,740,917	ss86334185	2424	652	2681	15788	26662	24049
29	44,807,928	ss117965824	20185	804	1305	37934	36739	26103
29	44,853,970	rs42192429	36290	112	19416	4118	21464	2705
29	44,900,940	rs43706228	1504	9	26793	43	35156	24021
29	44,969,518	ss86337154	21170	31013	35635	16801	23994	26608
29	44,979,377	ss86338214	24112	9928	13777	19335	30736	9711
29	44,999,264	ss86310727	143	1078	32294	2467	2164	425
29	45,023,665	ss86338763	25485	31014	30793	17900	23995	28945
29	45,102,557	ss86332221	170	2240	31730	75	31673	264
29	45,129,099	ss86335405	4960	2025	26978	5490	33645	24448
29	45,187,114	ss86295760	9892	468	16200	33586	24838	32136
29	45,287,502	ss86312485	7710	6287	36387	1294	30142	35470
29	45,326,585	rs42198683	23963	15047	6206	174	30801	14249
29	45,367,095	ss86322638	13328	12392	3940	22784	19051	6856
29	45,458,280	rs43706176	24499	6324	34840	34884	24588	40236
29	45,482,143	rs29025626	1893	136	35054	17005	2280	16790
29	45,530,264	ss86341375	34109	39453	35889	20334	18804	24973

¹UMD3.1 Coordinates. SNPs located within *CAST* and *CAPN1* are shaded in yellow.

²Commercialized SNPs are shaded in red.

³GBLUP allele substitution effect (α) ranks. Values less than 500 are shaded in yellow for the across-breed

⁴GBLUP of SNP allele substitution effects (α) estimated as a random effect.

⁵SNP allele substitution effects (β) estimated as fixed effects in a mixed linear model including the genome as a random effect.⁶-log₁₀(P)-value for the test of the null hypothesis of an allele substitution effect (β) of zero. Maximum va

⁷-log₁₀(P)-value for the test of the null hypothesis of all haplotype substitution effects (H) being zero. Max

⁸Number of haplotypes and effective number of haplotypes in parentheses for the 13 (*CAST*) or 31 (*CAPN*)

⁹Number Percentage of phenotypic variation in WBSF explained by haplotypes centered on the identified

						ASE ⁴		
BTA	POS ¹	SNP ID ²	α-All Breeds	α-Angus	α-Hereford	α-Charolais	α-Limousin	α-Simmental
7	97,151,592	rs41656985	0.00030671	-0.00017099	0.00020134	0.00017805	-0.00000025	0.00003928
7	97,261,052	rs41656987	0.00104868	0.00048033	0.00017963	-0.00001059	0.00011002	0.00011454
7	97,372,656	rs41570922	-0.00026557	-0.00024736	0.00001186	-0.00013418	-0.00004761	0.00001181
7	97,393,157	rs41615915	-0.00090198	0.00002637	-0.00048107	0.00000907	-0.00003997	-0.00007934
7	97,430,691	ss86295638	0.00074568	-0.00001324	0.00047692	-0.00012040	-0.00002678	0.00005340
7	97,501,859	ss86310801	-0.00039152	-0.00006694	-0.00012889	-0.00017279	0.00005665	-0.00004583
7	97,529,872	ss61472319	0.00045326	-0.00025686	0.00042590	-0.00019590	0.00007461	-0.00001851
7	97,691,853	ss86290016	0.00012060	0.00008623	0.00002409	0.00016817	0.00000658	-0.00002851
7	97,772,240	ss86312419	-0.00046509	-0.00038513	-0.00026961	-0.00010804	0.00004202	0.00000432
7	97,861,341	rs41593284	0.00097782	0.00011997	0.00031705	-0.00007204	0.00019796	0.00004403
7	97,898,940	rs41593281	0.00155220	0.00034795	0.00080756	0.00016613	0.00001148	0.00007858
7	97,961,659	ss117969141	0.00015075	0.00014493	0.00001131	0.00000912	0.00000444	0.00002638
7	98,013,150	ss117968909	0.00006102	-0.00010369	-0.00046716	0.00050154	0.00002137	0.00016343
7	98,173,299	ss86290989	0.00012363	0.00009822	-0.00022941	0.00049209	0.00001609	0.00001944
7	98,194,828	rs41658549	-0.00007628	-0.00045406	0.00038728	-0.00109154	0.00001558	0.00004740
7	98,254,815	rs41658542	0.00037965	-0.00015143	0.00060092	-0.00081707	-0.00005474	0.00003396
7	98,375,640	ss86329349	0.00085501	0.00051810	0.00043447	0.00001862	0.00002704	-0.00001097
7	98,495,888	rs43529872	0.00250806	0.00083827	0.00110064	0.00117126	0.00009663	-0.00003567
7	98,498,047	ss86321563	0.00251152	0.00094639	0.00113500	0.00114492	0.00007645	-0.00004943
7	98,538,952	rs41660170	0.00051614	0.00046201	-0.00000394	0.00034683	0.00001636	0.00003628
7	98,566,391	ss117962527	-0.00091729	-0.00063906	-0.00007139	-0.00081305	-0.00003279	0.00000133
7	98,579,574	rs41255587	0.00282846	0.00097459	0.00114941	0.00135049	0.00010269	-0.00002145
7	98,635,208	ss86300200	-0.00163961	-0.00033048	-0.00094817	0.00033141	-0.00008345	-0.00007121
7	98,646,770	rs41596489	0.00165452	0.00083405	0.00091620	0.00001794	0.00003965	0.00001667
7	98,680,293	ss86315737	-0.00122381	-0.00087793	-0.00080722	0.00022035	0.00004635	-0.00000223
7	98,726,055	rs29018251	0.00039725	-0.00079091	0.00029255	0.00047142	0.00000296	0.00002039
7	98,757,265	ss86303738	0.00031484	-0.00013005	0.00007134	0.00019325	-0.00000945	0.00008748
7	98,820,742	ss86324113	0.00133604	0.00080850	0.00064476	-0.00010404	-0.00002931	0.00011256
7	98,887,313	rs41568595	-0.00035467	0.00004527	-0.00006420	-0.00040082	0.00000383	-0.00001382
7	98,907,404	ss86291843	-0.00049765	-0.00001049	-0.00023992	-0.00019419	-0.00008403	0.00003096
7	98,974,456	ss86339659	0.00053311	0.00025554	0.00028576	0.00013611	0.00002468	0.00001069
7	99,024,444	ss117968912	-0.00020917	-0.00019566	0.00028752	-0.00066185	0.00004319	-0.00005451
7	99,085,299	rs41590403	-0.00048724	-0.00019597	0.00009020	-0.00037474	-0.00008357	-0.00001654
7	99,130,598	ss86333606	-0.00084381	0.00004792	-0.00082834	0.00005799	0.00001115	0.00006039
7	99,178,748	rs41568774	-0.00008141	-0.00004854	0.00014285	-0.00003014	-0.00004148	-0.00003983
7	99,215,474	ss86324013	0.00060578	0.00002168	0.00043622	-0.00002909	0.00000885	-0.00002556
7	99,344,820	rs41622872	-0.00089371	0.00019432	-0.00059364	0.00017413	-0.00010856	-0.00007464
7	99,399,852	ss117968895	0.00004348	-0.00022947	0.00011675	-0.00000801	-0.00000804	-0.00000512
7	99,492,904	ss86296856	-0.00059036	-0.00048595	-0.00029855	-0.00000510	-0.00000663	0.00000746
7	99,635,841	ss86339853	0.00010124	0.00004271	0.00022532	-0.00041791	0.00005579	-0.00007081
7	99,687,614	rs41657025	0.00027601	-0.00044383	0.00011698	0.00026276	-0.00000252	0.00008263
7	99,845,133	rs41624339	0.00087822	0.00010669	0.00041919	0.00028876	-0.00004153	0.00006660
7	99,919,908	ss86339607	0.00005831	-0.00007035	-0.00000100	0.00031240	0.00004996	-0.00003941
7	100,015,468	ss86310226	-0.00015773	0.00012360	-0.00002482	-0.00037122	0.00005151	-0.00004723
29	42,406,544	ss86319674	0.00004412	0.00050562	-0.00006947	-0.00016157	0.00003160	-0.00003943
29	42,455,680	ss117974470	-0.00023668	-0.00003069	0.00008615	0.00009795	-0.00007734	-0.00007606
29	42,620,218	rs42189770	0.00006534	0.00010962	-0.00011858	0.00039419	-0.00001053	-0.00001761
29	42,651,294	rs43706142	-0.00015187	-0.00070089	0.00012322	-0.00029180	0.00001081	0.00001108
29	42,696,595	rs42189112	0.00044366	0.00053810	-0.00019729	0.00082689	-0.00000348	0.00008903
29	42,749,808	rs29020063	-0.00015364	0.00030458	0.00006338	-0.00061076	0.00005270	-0.00012279
29	42,842,353	ss117974486	-0.00051136	-0.00047485	0.00025958	0.00014454	-0.00007630	-0.00023417
29	42,897,144	ss86322358	0.00016974	-0.00027606	0.00004743	0.00011962	-0.00001069	0.00007674

29	43,006,000	ss86339964	0.00009489	-0.00034623	0.00004546	0.00011962	-0.00001069	0.00006409
29	43,043,207	ss86341572	0.00026966	-0.00049034	0.00004519	0.00049483	-0.00005195	0.00009832
29	43,108,445	ss86337140	-0.00106080	-0.00067556	-0.00036196	-0.00021056	-0.00002031	-0.00007203
29	43,129,250	ss86337549	-0.00053788	-0.00077763	-0.00001082	-0.00002855	-0.00006132	-0.00003243
29	43,189,370	ss86319044	-0.00047528	-0.00077860	-0.00001082	-0.00001117	-0.00004383	-0.00003243
29	43,224,753	rs29013208	0.00048618	0.00073297	-0.00001707	-0.00011758	0.00004316	0.00006908
29	43,269,744	ss86282762	0.00032969	0.00063292	-0.00001988	-0.00014031	0.00003155	0.00002805
29	43,304,256	rs29024708	-0.00062896	-0.00068295	0.00012981	-0.00017576	-0.00001246	-0.00016043
29	43,328,607	ss86295061	0.00006312	0.00060219	-0.00022979	0.00033339	0.00002294	-0.00002393
29	43,429,511	ss86318094	-0.00160847	-0.00115096	-0.00079603	0.00019993	-0.00005774	-0.00007607
29	43,466,342	ss86310741	-0.00055100	-0.00078488	-0.00011944	-0.00031762	0.00007341	-0.00005915
29	43,498,073	ss86338800	0.00093454	0.00075831	0.00008009	0.00073932	-0.00005284	0.00009236
29	43,611,640	ss86298040	0.00146282	0.00030516	0.00040305	0.00095462	-0.00002067	0.00017820
29	43,652,252	ss86327310	-0.00118582	-0.00130334	-0.00027823	-0.00006298	-0.00004581	-0.00012680
29	43,686,401	ss86325323	-0.00012415	-0.00073056	-0.00022126	0.00033263	0.00000339	0.00004428
29	43,709,769	ss86290081	-0.00057947	-0.00100397	-0.00032111	0.00036105	0.00004399	-0.00004252
29	43,747,765	rs42190085	-0.00049735	-0.00020965	0.00001155	-0.00038731	-0.00002178	-0.00002225
29	43,749,527	ss86299346	-0.00019238	0.00016220	0.00001596	-0.00023397	-0.00000979	-0.00003480
29	43,777,249	ss86299989	-0.00006297	-0.00065114	-0.00002619	0.00022008	0.00000151	-0.00001811
29	43,826,144	rs42191289	0.00010758	0.00057745	-0.00022997	-0.00017228	-0.00006867	0.00017586
29	43,839,783	ss86336460	0.00061942	0.00081131	-0.00022565	0.00045409	-0.00003884	0.00020882
29	43,914,923	ss86335514	0.00178742	0.00045442	0.00036472	0.00105531	0.00006568	0.00019156
29	44,000,728	rs42191319	-0.00023431	0.00000024	-0.00020306	0.00014559	-0.00002916	0.00001428
29	44,029,526	rs42192038	-0.00092400	-0.00046153	-0.00009380	-0.00050894	-0.00003445	-0.00014690
29	44,042,363	rs42192064	-0.00185121	-0.00101148	-0.00035929	-0.00032758	0.00001350	-0.00033390
29	44,049,244	rs42192077	0.00051167	-0.00024213	0.00042010	0.00009658	-0.00000003	-0.00001236
29	44,050,471	ss86284058	-0.00072640	0.00013171	-0.00053768	-0.00038629	-0.00001074	0.00005388
29	44,051,567	rs42192079	-0.00044039	0.00017368	-0.00037741	-0.00009999	-0.00000151	0.00001440
29	44,053,733	rs42192083	0.00041510	-0.00023030	0.00038673	0.00007379	0.00000561	-0.00001662
29	44,054,901	rs42192084	0.00023354	-0.00015260	0.00019889	0.00029494	0.00001567	-0.00004086
29	44,058,688	rs42192090	0.00056930	0.00065475	-0.00014365	0.00097619	-0.00005793	0.00006581
29	44,060,410	rs42192096	-0.00052571	-0.00066766	0.00021685	-0.00076421	0.00003819	-0.00009649
29	44,062,694	rs42192100	-0.00050977	-0.00067190	0.00021482	-0.00070708	0.00003338	-0.00009162
29	44,063,938	rs17872078	-0.00295459	-0.00157336	-0.00080065	-0.00130368	-0.00001613	-0.00023251
29	44,067,234	rs17872093	0.00046438	0.00066766	-0.00027634	0.00076421	-0.00003338	0.00009915
29	44,067,796	rs17871984	0.00259095	0.00120226	0.00104514	0.00063915	0.00003574	0.00015159
29	44,068,143	rs17870631	0.00317238	0.00186992	0.00083717	0.00140771	0.00000236	0.00025628
29	44,068,346	rs17870628	0.00242209	0.00143725	0.00086741	0.00078922	-0.00002876	0.00016684
29	44,068,445	rs17870626	0.00308636	0.00178329	0.00081694	0.00138681	-0.00001299	0.00025696
29	44,068,519	rs17872010	0.00304194	0.00181486	0.00079066	0.00140771	0.00000236	0.00024530
29	44,068,580	rs17872004	0.00313874	0.00186992	0.00082829	0.00139445	0.00000629	0.00024985
29	44,068,812	rs17872003	-0.00312101	-0.00188257	-0.00082610	-0.00143916	0.00000748	-0.00024616
29	44,069,063	rs17812000	-0.00316072	-0.00228185	-0.00073880	-0.00140771	-0.00000236	-0.00024894
29	44,069,177	rs17872006	-0.00290630	-0.00194198	-0.00076244	-0.00120636	0.00002461	-0.00024429
29	44,070,713	rs42192103	-0.00332608	-0.00173409	-0.00094128	-0.00152269	0.00002317	-0.00028201
29	44,070,881	rs42192105	-0.00114491	-0.00046199	-0.00062239	-0.00008699	0.00000425	-0.00006435
29	44,071,034	rs42192107	-0.00110210	-0.00046869	-0.00062781	-0.00017354	0.00000425	-0.00003314
29	44,071,135	rs42192108	-0.00044909	-0.00004798	-0.00010125	-0.00018521	-0.00006208	-0.00000408
29	44,071,593	rs42192109	-0.00094890	-0.00100318	0.00008230	-0.00107584	0.00005396	-0.00010545
29	44,085,642	rs17871051	0.00181650	0.00134971	0.00024034	0.00077510	0.00009067	0.00018604
29	44,085,769	rs17871058	0.00236870	0.00130304	0.00021437	0.00146508	0.00018454	0.00021263
29	44,087,205	rs17872032	0.00096858	0.00059348	0.00002368	0.00061874	0.00004608	0.00010203
29	44,087,356	rs17872033	-0.00172481	-0.00132279	-0.00023887	-0.00074441	-0.00010755	-0.00016116
29	44,087,629	rs17872050	0.00241788	0.00143400	0.00021062	0.00148598	0.00019989	0.00020641
29	44,087,858	rs17872151	0.00053210	-0.00001758	0.00011545	0.00030835	0.00002839	0.00003877

29	44,088,897	rs17870847	-0.00236640	-0.00134853	-0.00018849	-0.00152169	-0.00019782	-0.00019442
29	44,110,295	rs42192119	-0.00020159	0.00009268	-0.00003017	-0.00033493	-0.00003855	0.00001843
29	44,119,671	rs42195143	0.00016832	-0.00029353	0.00040275	-0.00006054	0.00001746	-0.00002797
29	44,122,272	rs42194216	-0.00031009	0.00011168	-0.00025424	-0.00012528	0.00001347	-0.00000075
29	44,125,747	rs42194178	-0.00032379	0.00014293	-0.00028060	-0.00012467	0.00001347	-0.00000075
29	44,130,887	rs42194132	0.00025708	-0.00014293	0.00026202	0.00012655	-0.00001347	-0.00001560
29	44,154,126	rs42193349	-0.00039133	0.00036022	-0.00029871	-0.00007837	0.00001820	-0.00003331
29	44,172,614	ss117965984	-0.00069936	0.00000948	-0.00031668	-0.00035165	0.00002555	-0.00008372
29	44,196,154	ss86318958	0.00014359	0.00029049	0.00024258	-0.00017471	0.00000858	-0.00001230
29	44,208,978	rs29003633	0.00027473	0.00067584	0.00000504	0.00005976	-0.00000215	-0.00002063
29	44,223,148	ss86323783	0.00095480	0.00108636	0.00002128	0.00075592	0.00006222	0.00002016
29	44,243,444	ss86313099	-0.00010319	0.00085706	-0.00056913	0.00050513	0.00001353	-0.00003883
29	44,325,408	ss86292140	-0.00161978	-0.00161585	-0.00017661	-0.00061998	-0.00004278	-0.00014539
29	44,372,611	ss86329852	-0.00035147	0.00002025	-0.00012224	-0.00059268	-0.00006096	0.00007161
29	44,395,075	ss86333994	-0.00120791	-0.00077009	-0.00038065	0.00006199	-0.00002805	-0.00017409
29	44,416,282	rs43709648	-0.00203603	-0.00103453	-0.00093446	-0.00067339	-0.00001133	-0.00005219
29	44,546,564	ss86288185	0.00110217	0.00069894	0.00045516	0.00051185	-0.00000784	0.00005656
29	44,585,782	ss86341172	-0.00075142	-0.00059974	-0.00022848	-0.00066809	0.00004126	-0.00004148
29	44,628,137	rs41600300	-0.00005648	0.00034145	0.00005371	0.00013032	-0.00004817	-0.00003908
29	44,649,908	ss86337530	0.00005313	-0.00008978	0.00038621	-0.00022923	0.00001713	-0.00009300
29	44,740,917	ss86334185	0.00079430	0.00082804	0.00038222	-0.00025986	0.00002142	0.00002880
29	44,807,928	ss117965824	-0.00026913	0.00079928	-0.00045557	0.00002440	0.00000569	0.00002481
29	44,853,970	rs42192429	0.00005315	-0.00107690	0.00013023	-0.00052061	0.00003071	0.00010706
29	44,900,940	rs43706228	0.00089149	0.00166157	-0.00007800	0.00120207	-0.00000796	-0.00002885
29	44,969,518	ss86337154	-0.00025376	-0.00008685	0.00002682	-0.00024640	-0.00002614	-0.00002386
29	44,979,377	ss86338214	0.00021114	0.00036588	-0.00018187	0.00021199	0.00001482	0.00006627
29	44,999,264	ss86310727	0.00133191	0.00075573	0.00004545	0.00060918	0.00010639	0.00015623
29	45,023,665	ss86338763	-0.00019088	-0.00008685	0.00005425	-0.00023066	-0.00002614	-0.00001956
29	45,102,557	ss86332221	-0.00129469	-0.00064203	-0.00004862	-0.00111294	0.00001335	-0.00016787
29	45,129,099	ss86335405	0.00063776	0.00065799	0.00007693	0.00047129	0.00001030	0.00002804
29	45,187,114	ss86295760	-0.00047535	-0.00087672	-0.00015742	-0.00006285	-0.00002459	0.00001400
29	45,287,502	ss86312485	0.00053477	0.00045858	0.00002288	0.00071079	0.00001575	-0.00000847
29	45,326,585	rs42198683	0.00021305	0.00027334	-0.00028774	0.00099702	0.00001472	-0.00005160
29	45,367,095	ss86322638	0.00039329	0.00031861	0.00033922	-0.00017070	0.00003571	-0.00007839
29	45,458,280	rs43706176	-0.00020553	-0.00045743	0.00003098	-0.00005162	-0.00002502	0.00000069
29	45,482,143	rs29025626	-0.00084208	-0.00104550	-0.00002985	-0.00024322	-0.00010494	-0.00004481
29	45,530,264	ss86341375	0.00019820	0.00005755	0.00002545	-0.00001078	0.00003298	0.00003977

¹UMD3.1 Coordinates. SNPs located within *CAST* and *CAPN1* are shaded in yellow.

²Commercialized SNPs are shaded in red.

³GBLUP allele substitution effect (α) ranks. Values less than 500 are shaded in yellow for the across-breed and green for the within-

⁴GBLUP of SNP allele substitution effects (α) estimated as a random effect.

⁵SNP allele substitution effects (β) estimated as fixed effects in a mixed linear model including the genomic relationship matrix.

⁶ $-\log_{10}(P)$ -value for the test of the null hypothesis of an allele substitution effect (β) of zero. Maximum values are shaded in red. Oth

⁷ $-\log_{10}(P)$ -value for the test of the null hypothesis of all haplotype substitution effects (H) being zero. Maximum values are shaded i

⁸Number of haplotypes and effective number of haplotypes in parentheses for the 13 (*CAST*) or 31 (*CAPN1*) SNP block centered on

⁹Number Percentage of phenotypic variation in WBSF explained by haplotypes centered on the identified SNP.

						ASE ⁵		
BTA	POS ¹	SNP ID ²	β-All Breeds	β-Angus	β-Hereford	β-Charolais	β-Limousin	β-Simmental
7	97,151,592	rs41656985	0.01377207	-0.01999276	0.03740770	0.01615795	-0.00029396	0.03399697
7	97,261,052	rs41656987	0.06407879	0.08585839	0.05622007	-0.00113931	0.15788787	0.11469922
7	97,372,656	rs41570922	-0.04721657	-0.10888501	0.02478650	-0.03871002	-0.15544713	0.02536908
7	97,393,157	rs41615915	-0.04605863	0.00265377	-0.10743993	0.00108729	-0.05573660	-0.07783973
7	97,430,691	ss86295638	0.05460805	-0.00518239	0.10506659	-0.02294942	-0.04461769	0.07698709
7	97,501,859	ss86310801	-0.03764247	-0.02495779	-0.04955234	-0.03468353	0.08999742	-0.09143018
7	97,529,872	ss61472319	0.02111581	-0.02877606	0.08140793	-0.01884309	0.10324757	-0.01642583
7	97,691,853	ss86290016	0.04112449	0.13325936	0.05822260	0.12703600	0.04074417	-0.09219867
7	97,772,240	ss86312419	-0.05640512	-0.07610179	-0.21729369	-0.02281948	0.30240522	0.00927325
7	97,861,341	rs41593284	0.05750871	0.01407221	0.11133231	-0.00899134	0.24638150	0.04204862
7	97,898,940	rs41593281	0.09632991	0.07850543	0.14152236	0.04174867	0.01595788	0.08909754
7	97,961,659	ss117969141	0.04610124	0.12701127	0.01169940	0.00594871	0.04862822	0.17698328
7	98,013,150	ss117968909	0.00300209	-0.01193793	-0.09714359	0.05201490	0.02690835	0.15605575
7	98,173,299	ss86290989	0.00767338	0.01261753	-0.06474281	0.07826779	0.01956097	0.02321594
7	98,194,828	rs41658549	-0.00401437	-0.04982220	0.09135510	-0.13132990	0.02229160	0.04134878
7	98,254,815	rs41658542	0.02188950	-0.01574779	0.20327112	-0.10260593	-0.07012338	0.03239528
7	98,375,640	ss86329349	0.09183851	0.12926199	0.20569660	0.00380099	0.11857929	-0.02275644
7	98,495,888	rs43529872	0.14912943	0.12638542	0.20438144	0.18318184	0.24750333	-0.03846871
7	98,498,047	ss86321563	0.14221431	0.15154723	0.20916753	0.15264208	0.18729389	-0.04713413
7	98,538,952	rs41660170	0.07895436	0.13526771	-0.00409153	0.08051120	0.07729644	0.11766511
7	98,566,391	ss117962527	-0.09262624	-0.16100475	-0.06040231	-0.16610346	-0.05483045	0.00153287
7	98,579,574	rs41255587	0.15449911	0.14576743	0.21255338	0.19065204	0.14454926	-0.02075111
7	98,635,208	ss86300200	-0.07152941	-0.03340736	-0.16969513	0.03199936	-0.10216313	-0.05727451
7	98,646,770	rs41596489	0.08027895	0.08287525	0.18982409	0.00170165	0.06672588	0.01508636
7	98,680,293	ss86315737	-0.05859165	-0.10106432	-0.15573983	0.02425142	0.06258840	-0.00192055
7	98,726,055	rs29018251	0.02359443	-0.12618996	0.07884128	0.05065498	0.00635118	0.01937443
7	98,757,265	ss86303738	0.02532671	-0.01615925	0.05567595	0.03238808	-0.01262411	0.11054776
7	98,820,742	ss86324113	0.07294052	0.08716323	0.17291781	-0.01161769	-0.05684945	0.10538010
7	98,887,313	rs41568595	-0.03694200	0.01652002	-0.02094997	-0.18933093	0.00660686	-0.02603140
7	98,907,404	ss86291843	-0.02347963	-0.00112256	-0.03939083	-0.02093560	-0.12977007	0.03256895
7	98,974,456	ss86339659	0.02520614	0.02355067	0.04765437	0.01524006	0.04806978	0.01211776
7	99,024,444	ss117968912	-0.00962625	-0.02314016	0.04887861	-0.06772105	0.06137752	-0.05045382
7	99,085,299	rs41590403	-0.03960914	-0.05700088	0.02546463	-0.07769533	-0.22934220	-0.01881188
7	99,130,598	ss86333606	-0.06239241	0.00956325	-0.14975990	0.02080513	0.03399904	0.11373474
7	99,178,748	rs41568774	-0.00494952	-0.00595571	0.04305756	-0.00422053	-0.06928228	-0.03732380
7	99,215,474	ss86324013	0.03866208	0.00323942	0.13672049	-0.00375089	0.01211855	-0.03134186
7	99,344,820	rs41622872	-0.04295510	0.02002393	-0.12011580	0.01951865	-0.13440981	-0.07138409
7	99,399,852	ss117968895	0.00566668	-0.05979255	0.05792219	-0.00246880	-0.06191476	-0.01295397
7	99,492,904	ss86296856	-0.06625218	-0.10116761	-0.17772993	-0.00151215	-0.01224771	0.01697012
7	99,635,841	ss86339853	0.00560736	0.00581627	0.05035461	-0.05124237	0.08750034	-0.07198733
7	99,687,614	rs41657025	0.01600630	-0.05598055	0.03944556	0.02693623	-0.00419388	0.07459634
7	99,845,133	rs41624339	0.05420017	0.01451857	0.08271281	0.04128013	-0.15385321	0.10367658
7	99,919,908	ss86339607	0.00320745	-0.00812169	-0.00021135	0.05011518	0.06678217	-0.03988769
7	100,015,468	ss86310226	-0.00884300	0.01313929	-0.00799969	-0.04322683	0.07312651	-0.04484400
29	42,406,544	ss86319674	0.00499755	0.13127994	-0.02539683	-0.05011073	0.37427564	-0.07250370
29	42,455,680	ss117974470	-0.01114205	-0.00287066	0.01625321	0.01350677	-0.08903101	-0.06311767
29	42,620,218	rs42189770	0.00437862	0.01893309	-0.02713130	0.07412626	-0.02035679	-0.02046697
29	42,651,294	rs43706142	-0.00912868	-0.07832798	0.04644727	-0.03432996	0.01516783	0.01150035
29	42,696,595	rs42189112	0.02244031	0.06801028	-0.03648918	0.10811249	-0.00408642	0.08595896
29	42,749,808	rs29020063	-0.00802797	0.03088923	0.01431881	-0.08214113	0.06422537	-0.11007124
29	42,842,353	ss117974486	-0.02723432	-0.05483318	0.06254769	0.01804422	-0.09758154	-0.20088805
29	42,897,144	ss86322358	0.01390338	-0.04068813	0.02886829	0.01772594	-0.01746038	0.10763037

29	43,006,000	ss86339964	0.00786039	-0.05214215	0.02769884	0.01772594	-0.01746038	0.09288296
29	43,043,207	ss86341572	0.01905446	-0.06102574	0.02423195	0.06732475	-0.08042507	0.10649011
29	43,108,445	ss86337140	-0.09515691	-0.18767192	-0.13426794	-0.05009274	-0.03198651	-0.10713556
29	43,129,250	ss86337549	-0.11213504	-0.36449310	-0.05938852	-0.01576700	-0.11245798	-0.07599159
29	43,189,370	ss86319044	-0.09177632	-0.35818174	-0.05938852	-0.00449407	-0.08165142	-0.07599159
29	43,224,753	rs29013208	0.07685161	0.23681481	-0.06367290	-0.03767127	0.07834478	0.13411425
29	43,269,744	ss86282762	0.06673067	0.22340633	-0.08516222	-0.04797645	0.06672672	0.13893634
29	43,304,256	rs29024708	-0.05533914	-0.18017752	0.05280083	-0.03602372	-0.02059741	-0.21167262
29	43,328,607	ss86295061	0.00409931	0.06677072	-0.08406764	0.05513809	0.03738891	-0.02303009
29	43,429,511	ss86318094	-0.08927452	-0.11940061	-0.19002689	0.02397019	-0.17416374	-0.07217357
29	43,466,342	ss86310741	-0.05527207	-0.18298300	-0.03897509	-0.08345126	0.21664736	-0.15334543
29	43,498,073	ss86338800	0.05956164	0.11996911	0.01582097	0.12870934	-0.13744882	0.12546311
29	43,611,640	ss86298040	0.07322512	0.03240417	0.07923634	0.11566400	-0.02602530	0.17796485
29	43,652,252	ss86327310	-0.05350543	-0.13120156	-0.04690503	-0.00705293	-0.05862478	-0.10243448
29	43,686,401	ss86325323	-0.01025002	-0.12481137	-0.05790675	0.07998412	0.02080392	0.07436958
29	43,709,769	ss86290081	-0.03614715	-0.09808855	-0.14603245	0.04284288	0.06642355	-0.04706384
29	43,747,765	rs42190085	-0.03252887	-0.03454110	0.00266994	-0.06688717	-0.03643018	-0.02716611
29	43,749,527	ss86299346	-0.01815565	0.04194873	0.00506304	-0.04813533	-0.07093084	-0.05943258
29	43,777,249	ss86299989	-0.00379751	-0.08865721	-0.00587409	0.03403038	0.00214447	-0.02166572
29	43,826,144	rs42191289	0.00538920	0.08261932	-0.04308125	-0.01792714	-0.10331144	0.16352930
29	43,839,783	ss86336460	0.02873918	0.09722623	-0.03889303	0.04674230	-0.05443953	0.17591056
29	43,914,923	ss86335514	0.14099316	0.12325906	0.11582581	0.17858418	0.10103476	0.27239461
29	44,000,728	rs42191319	-0.02134130	0.00009678	-0.04485603	0.05849863	-0.10881374	0.02442284
29	44,029,526	rs42192038	-0.04465678	-0.04790513	-0.01687600	-0.05861484	-0.06926916	-0.12931805
29	44,042,363	rs42192064	-0.09088154	-0.11220353	-0.06259312	-0.03927838	0.01761857	-0.31307293
29	44,049,244	rs42192077	0.02578055	-0.02692225	0.08254911	0.01055042	-0.00004142	-0.01123121
29	44,050,471	ss86284058	-0.06361724	0.02388787	-0.19851647	-0.07943526	-0.02527633	0.08868873
29	44,051,567	rs42192079	-0.02210319	0.01920409	-0.07340928	-0.01089515	-0.00185196	0.01290773
29	44,053,733	rs42192083	0.02086679	-0.02545535	0.07588543	0.00806255	0.00679728	-0.01483180
29	44,054,901	rs42192084	0.01512321	-0.02258374	0.04596259	0.04186951	0.02413509	-0.05674960
29	44,058,688	rs42192090	0.02968789	0.06906875	-0.02816224	0.11941891	-0.07838293	0.05512612
29	44,060,410	rs42192096	-0.02832327	-0.07343302	0.04272696	-0.09131420	0.06035150	-0.08307020
29	44,062,694	rs42192100	-0.02736293	-0.07396977	0.04226760	-0.08474445	0.05322737	-0.07665678
29	44,063,938	rs17872078	-0.18564305	-0.18455479	-0.20510618	-0.16345367	-0.03249970	-0.23021449
29	44,067,234	rs17872093	0.02496105	0.07343302	-0.05406733	0.09131420	-0.05322737	0.08515734
29	44,067,796	rs17871984	0.17226965	0.20960280	0.25854084	0.10460733	0.08033891	0.14060072
29	44,068,143	rs17870631	0.23869986	0.22119704	0.24379122	0.22023146	0.00547252	0.34767985
29	44,068,346	rs17870628	0.16042843	0.15402954	0.24841222	0.10918790	-0.05396674	0.19102806
29	44,068,445	rs17870626	0.22829997	0.21152447	0.23663609	0.21618169	-0.02950121	0.32679359
29	44,068,519	rs17872010	0.22980629	0.21678554	0.23000251	0.22023146	0.00547252	0.33560285
29	44,068,580	rs17872004	0.23576592	0.22119704	0.24158328	0.21914000	0.01402673	0.33693156
29	44,068,812	rs17872003	-0.23425299	-0.22039076	-0.24087221	-0.22570015	0.01719659	-0.33744060
29	44,069,063	rs17812000	-0.23938706	-0.27604109	-0.21680105	-0.22023146	-0.00547252	-0.33888089
29	44,069,177	rs17872006	-0.20865952	-0.22809167	-0.21525294	-0.17836251	0.05335006	-0.31640257
29	44,070,713	rs42192103	-0.23126101	-0.20077133	-0.25377584	-0.23262707	0.04616506	-0.33919363
29	44,070,881	rs42192105	-0.13150092	-0.09916322	-0.20618399	-0.03162694	0.02776421	-0.16146931
29	44,071,034	rs42192107	-0.14426575	-0.11047033	-0.21343493	-0.07328780	0.02776421	-0.16118552
29	44,071,135	rs42192108	-0.05688668	-0.02886829	-0.03653651	-0.04193928	-0.29972195	-0.02004771
29	44,071,593	rs42192109	-0.05027538	-0.10884482	0.01585778	-0.12844689	0.08759822	-0.09627713
29	44,085,642	rs17871051	0.14188557	0.30364766	0.10809754	0.11126940	0.13503153	0.20082779
29	44,085,769	rs17871058	0.14392345	0.15281348	0.06846588	0.18131448	0.28735643	0.19762528
29	44,087,205	rs17872032	0.18873706	0.25640780	0.03850535	0.20027467	0.15725079	0.30972904
29	44,087,356	rs17872033	-0.12775860	-0.27170879	-0.10219163	-0.10479101	-0.15498932	-0.15942987
29	44,087,629	rs17872050	0.14442059	0.16563130	0.06653446	0.18413259	0.30762227	0.17956041
29	44,087,858	rs17872151	0.14001255	-0.02272857	0.30154212	0.12323939	0.07713691	0.18930825

29	44,088,897	rs17870847	-0.14124160	-0.15463556	-0.05878994	-0.18885633	-0.30340823	-0.17524866
29	44,110,295	rs42192119	-0.01942996	0.01451903	-0.02155698	-0.06463021	-0.08669320	0.03046439
29	44,119,671	rs42195143	0.00783300	-0.02935938	0.07389328	-0.00669293	0.02115000	-0.02711373
29	44,122,272	rs42194216	-0.03172111	0.02819610	-0.08098997	-0.04973577	0.02964052	-0.00160258
29	44,125,747	rs42194178	-0.03356792	0.03659072	-0.09186858	-0.04942879	0.02964052	-0.00160258
29	44,130,887	rs42194132	0.02644605	-0.03659072	0.08421906	0.05072096	-0.02964052	-0.03311083
29	44,154,126	rs42193349	-0.05305730	0.22356813	-0.10323256	-0.05776275	0.04588778	-0.09831775
29	44,172,614	ss117965984	-0.03964292	0.00112919	-0.06918327	-0.04362937	0.04977295	-0.10354199
29	44,196,154	ss86318958	0.01564406	0.11621015	0.08928295	-0.04546044	0.03894493	-0.02006039
29	44,208,978	rs29003633	0.07439988	0.43869793	0.00575558	0.03243145	-0.04998931	-0.08817917
29	44,223,148	ss86323783	0.07582241	0.21702321	0.00803405	0.12606020	0.13368766	0.02592427
29	44,243,444	ss86313099	-0.00549653	0.11812362	-0.10476431	0.08059616	0.02143301	-0.03460116
29	44,325,408	ss86292140	-0.16398496	-0.20530041	-0.19003334	-0.12468567	-0.10603965	-0.24574655
29	44,372,611	ss86329852	-0.03713291	0.00488436	-0.08660821	-0.09708762	-0.17343672	0.13482641
29	44,395,075	ss86333994	-0.06754849	-0.10992804	-0.09616456	0.00711078	-0.03712152	-0.16178806
29	44,416,282	rs43709648	-0.13069556	-0.28351741	-0.18944356	-0.09438042	-0.01593376	-0.08385696
29	44,546,564	ss86288185	0.05494993	0.09262489	0.08928476	0.05312496	-0.01034263	0.05095507
29	44,585,782	ss86341172	-0.03866292	-0.06206035	-0.05039949	-0.08198585	0.06203462	-0.03992657
29	44,628,137	rs41600300	-0.01483796	0.20889018	0.15455551	0.06038629	-0.18452356	-0.14991919
29	44,649,908	ss86337530	0.00294146	-0.01196893	0.08771622	-0.02822089	0.02041584	-0.09897733
29	44,740,917	ss86334185	0.05012176	0.10695692	0.08835503	-0.03612618	0.10055830	0.03904043
29	44,807,928	ss117965824	-0.01428477	0.10722949	-0.08601306	0.00337124	0.00765424	0.02422262
29	44,853,970	rs42192429	0.00310823	-0.14208317	0.02747885	-0.07932534	0.06115144	0.11080152
29	44,900,940	rs43706228	0.04401726	0.16432737	-0.01507454	0.14127813	-0.01453902	-0.02478305
29	44,969,518	ss86337154	-0.08569177	-0.09080754	0.27706137	-0.16974889	-0.08763089	-0.07547633
29	44,979,377	ss86338214	0.00973100	0.03288093	-0.03428688	0.02287154	0.02023673	0.05906225
29	44,999,264	ss86310727	0.07636034	0.08409333	0.01064296	0.09008127	0.16345165	0.16162329
29	45,023,665	ss86338763	-0.06266468	-0.09080754	0.56904494	-0.14493435	-0.08763089	-0.06060103
29	45,102,557	ss86332221	-0.09128831	-0.10489015	-0.01759630	-0.20456570	0.01847027	-0.16251600
29	45,129,099	ss86335405	0.11751600	0.15237997	0.16724531	0.20802589	0.03794230	0.08782773
29	45,187,114	ss86295760	-0.02403866	-0.10408408	-0.03232491	-0.00787294	-0.03145318	0.01223186
29	45,287,502	ss86312485	0.09994421	0.09989672	0.05326782	0.21938837	0.26063282	-0.02542529
29	45,326,585	rs42198683	0.01064705	0.03273957	-0.05642473	0.10167291	0.02256656	-0.05231106
29	45,367,095	ss86322638	0.02307329	0.03872453	0.09838548	-0.01799483	0.09863873	-0.08139580
29	45,458,280	rs43706176	-0.02873231	-0.11397784	0.07484033	-0.01161712	-0.08531336	0.00126990
29	45,482,143	rs29025626	-0.05831395	-0.18623897	-0.00657759	-0.04365267	-0.32231770	-0.06272849
29	45,530,264	ss86341375	0.02131837	0.05111941	0.00589401	-0.00306374	0.15679441	0.20788969

¹UMD3.1 Coordinates. SNPs located within *CAST* and *CAPN1* are shaded in yellow.

²Commercialized SNPs are shaded in red.

³GBLUP allele substitution effect (α) ranks. Values less than 500 are shaded in yellow for the across-breed and green for the within-breed.

⁴GBLUP of SNP allele substitution effects (α) estimated as a random effect.

⁵SNP allele substitution effects (β) estimated as fixed effects in a mixed linear model including the genomic relationship matrix.

⁶ $-\log_{10}(P)$ -value for the test of the null hypothesis of an allele substitution effect (β) of zero. Maximum values are shaded in red. Of

⁷ $-\log_{10}(P)$ -value for the test of the null hypothesis of all haplotype substitution effects (H) being zero. Maximum values are shaded

⁸Number of haplotypes and effective number of haplotypes in parentheses for the 13 (*CAST*) or 31 (*CAPN1*) SNP block centered on the

⁹Number Percentage of phenotypic variation in WBSF explained by haplotypes centered on the identified SNP.

						-log ₁₀ (P)ASE ⁶		
BTA	POS ¹	SNP ID ²	β-All Breeds	β-Angus	β-Hereford	β-Charolais	β-Limousin	β-Simmental
7	97,151,592	rs41656985	0.25920819	0.19065791	0.38791104	0.17268288	0.00129203	0.24547389
7	97,261,052	rs41656987	1.76394501	0.96309267	0.46932913	0.00960706	1.15663403	1.13658381
7	97,372,656	rs41570922	0.51757650	0.70940830	0.06022060	0.24466141	0.62472795	0.10403711
7	97,393,157	rs41615915	1.21374534	0.02346959	1.51546840	0.00867879	0.28640193	0.65871607
7	97,430,691	ss86295638	1.19548289	0.02323031	1.47921826	0.16870415	0.19703810	0.49965269
7	97,501,859	ss86310801	0.57707351	0.12657802	0.34928548	0.26680432	0.48566729	0.50598038
7	97,529,872	ss61472319	0.43312604	0.30306271	1.11617585	0.19968551	0.64220544	0.10489070
7	97,691,853	ss86290016	0.28588801	0.40039921	0.14156066	0.60508426	0.08498000	0.37342394
7	97,772,240	ss86312419	0.86395033	0.75292586	1.67261725	0.15800490	0.91674896	0.03562833
7	97,861,341	rs41593284	1.53245331	0.12732425	1.13126148	0.07533843	2.64951708	0.29967328
7	97,898,940	rs41593281	3.42270182	0.71645917	2.89390082	0.29177371	0.06921540	0.71900816
7	97,961,659	ss117969141	0.35277075	0.54610435	0.03956972	0.02062259	0.07559241	0.54397980
7	98,013,150	ss117968909	0.04524314	0.10712272	1.36976476	0.69474730	0.12949977	1.90813017
7	98,173,299	ss86290989	0.10943140	0.10718998	0.60809591	0.91744683	0.09275246	0.13070592
7	98,194,828	rs41658549	0.05932558	0.62843426	1.13325108	2.56758808	0.09789700	0.31044044
7	98,254,815	rs41658542	0.39532965	0.15482480	3.06228709	1.65770810	0.40341524	0.21863565
7	98,375,640	ss86329349	1.99903332	1.38818084	2.35512143	0.02362894	0.35954871	0.09411136
7	98,495,888	rs43529872	7.74766418	1.99768902	5.22892170	3.62427416	1.47999444	0.24953504
7	98,498,047	ss86321563	7.42639931	2.56544376	5.48906355	3.03632723	1.00081075	0.34592414
7	98,538,952	rs41660170	1.19616937	1.31606193	0.01343470	0.72869343	0.20372510	0.51234229
7	98,566,391	ss117962527	2.13133465	1.95083162	0.27369699	2.44272959	0.25132133	0.00778098
7	98,579,574	rs41255587	8.94616131	2.54505254	5.63316775	4.25399597	1.02795263	0.12970451
7	98,635,208	ss86300200	2.78390969	0.39024136	3.88488884	0.38083683	0.68919867	0.49697830
7	98,646,770	rs41596489	3.09302733	1.42263877	4.15919781	0.01538183	0.31858437	0.09451937
7	98,680,293	ss86315737	1.85792616	1.73175280	3.13848683	0.24889004	0.33750113	0.01134466
7	98,726,055	rs29018251	0.42728013	1.90332787	0.82779401	0.65329731	0.02111718	0.12131636
7	98,757,265	ss86303738	0.38498763	0.14407068	0.26033788	0.27396792	0.05509740	0.90591284
7	98,820,742	ss86324113	2.38541310	1.44419614	2.83381698	0.10584866	0.24004092	1.05287378
7	98,887,313	rs41568595	0.53301860	0.08132593	0.13823755	1.53243070	0.02459171	0.11513550
7	98,907,404	ss86291843	0.49381227	0.00947962	0.44931494	0.21138458	0.82054150	0.20763072
7	98,974,456	ss86339659	0.54215062	0.26713043	0.57315687	0.14318927	0.19621006	0.06602532
7	99,024,444	ss117968912	0.16733868	0.22504722	0.58555919	1.02559764	0.31898397	0.38434202
7	99,085,299	rs41590403	0.69481474	0.39318251	0.18795130	0.75050635	1.24660458	0.10624050
7	99,130,598	ss86333606	1.45570588	0.06251611	3.10294183	0.10574727	0.10273524	0.70938049
7	99,178,748	rs41568774	0.06868082	0.04898987	0.34108982	0.03196463	0.33551761	0.26193372
7	99,215,474	ss86324013	0.79647808	0.02351372	1.69652140	0.02952516	0.05206018	0.18142548
7	99,344,820	rs41622872	1.14352553	0.20570883	1.95773851	0.19025349	1.01497461	0.59501667
7	99,399,852	ss117968895	0.05287460	0.44925767	0.36214999	0.01233920	0.11948527	0.04633037
7	99,492,904	ss86296856	1.15969824	1.09708746	1.54697553	0.00766042	0.04497447	0.06521665
7	99,635,841	ss86339853	0.08261138	0.04523761	0.50695580	0.60607729	0.47188976	0.57737955
7	99,687,614	rs41657025	0.26637232	0.67054698	0.28528814	0.29544248	0.01572183	0.65781175
7	99,845,133	rs41624339	1.34660053	0.12133397	1.11618627	0.41055563	0.56501728	0.71205727
7	99,919,908	ss86339607	0.04573644	0.07034137	0.00151539	0.49076674	0.36871254	0.27101227
7	100,015,468	ss86310226	0.13573436	0.12458893	0.04893090	0.49885840	0.39851707	0.32578504
29	42,406,544	ss86319674	0.04986806	1.37866264	0.16134861	0.32115619	0.87009257	0.39403172
29	42,455,680	ss117974470	0.19574411	0.02641378	0.14141656	0.11127875	0.59456400	0.55434182
29	42,620,218	rs42189770	0.05722611	0.14305650	0.22931731	0.75240467	0.07529309	0.11527340
29	42,651,294	rs43706142	0.13527357	1.19216972	0.32601885	0.36725161	0.06524151	0.06544274
29	42,696,595	rs42189112	0.44441091	0.88270802	0.37685810	1.74463604	0.01829748	0.76562942
29	42,749,808	rs29020063	0.12666589	0.35244490	0.11091297	1.11550797	0.37213472	1.16115545
29	42,842,353	ss117974486	0.55536657	0.69280424	0.64651365	0.16318906	0.62728700	3.18305827
29	42,897,144	ss86322358	0.18345331	0.39458459	0.13964490	0.14498396	0.06992430	0.80845199

29	43,006,000	ss86339964	0.09586061	0.53898948	0.13318280	0.14498396	0.06992430	0.64216062
29	43,043,207	ss86341572	0.29218063	0.76407239	0.12313821	0.82608844	0.42613324	0.96006708
29	43,108,445	ss86337140	2.45598566	2.31486819	1.44440671	0.37952271	0.13871960	0.77016154
29	43,129,250	ss86337549	1.61915754	4.63029649	0.09175169	0.06199632	0.59514087	0.35844100
29	43,189,370	ss86319044	1.25955168	4.56366938	0.09175169	0.01982073	0.38561856	0.35844100
29	43,224,753	rs29013208	1.12052175	3.01526390	0.12262529	0.22241437	0.37189194	0.87811532
29	43,269,744	ss86282762	0.76185346	2.53505836	0.15756175	0.28646199	0.27662167	0.48219951
29	43,304,256	rs29024708	1.06275615	2.25837870	0.36526377	0.27590072	0.08300408	2.41431365
29	43,328,607	ss86295061	0.05426188	0.94535620	0.72983337	0.54636948	0.16252304	0.14634925
29	43,429,511	ss86318094	3.30593304	2.47535623	3.68132176	0.23311529	0.77433371	0.60737632
29	43,466,342	ss86310741	0.96296598	2.56839941	0.28684653	0.70252500	1.08226275	0.86478838
29	43,498,073	ss86338800	1.52028312	1.76670225	0.13365834	1.83411013	0.61664702	1.03469542
29	43,611,640	ss86298040	2.58028835	0.36374051	1.04977109	2.06890532	0.12475821	2.28082929
29	43,652,252	ss86327310	1.68525775	2.97699466	0.55688163	0.06156001	0.32155822	1.12682579
29	43,686,401	ss86325323	0.12890225	1.76992464	0.55000156	0.70435872	0.04177780	0.43177499
29	43,709,769	ss86290081	0.73588744	1.88286213	1.40490730	0.48685638	0.33902519	0.31447126
29	43,747,765	rs42190085	0.61498554	0.29925040	0.01867855	0.69135855	0.15545894	0.15423447
29	43,749,527	ss86299346	0.23117133	0.28797421	0.03062952	0.39580652	0.14410590	0.32099723
29	43,777,249	ss86299989	0.05204709	1.23855542	0.04279939	0.30596175	0.00862948	0.12086964
29	43,826,144	rs42191289	0.08355832	1.07275064	0.46344422	0.17992963	0.60679991	2.10421872
29	43,839,783	ss86336460	0.65687172	1.57750548	0.42813638	0.60240929	0.27736123	2.57848708
29	43,914,923	ss86335514	5.41309793	1.21043891	1.29638005	3.23934367	0.57977131	3.48219782
29	44,000,728	rs42191319	0.28733855	0.00041707	0.43862251	0.33148269	0.35713837	0.11318397
29	44,029,526	rs42192038	1.20751437	0.61860399	0.15163110	0.76352207	0.29883743	1.50891107
29	44,042,363	rs42192064	3.78983596	2.11305517	0.81294077	0.43141451	0.07967046	6.51065616
29	44,049,244	rs42192077	0.53544650	0.28049136	1.11635461	0.09636135	0.00017937	0.06853338
29	44,050,471	ss86284058	1.31634950	0.18165119	2.73155940	0.77897574	0.08559228	0.55261272
29	44,051,567	rs42192079	0.43791985	0.18793165	0.94534508	0.09995925	0.00801219	0.08018721
29	44,053,733	rs42192083	0.40600605	0.26290107	0.98615509	0.07197118	0.03036354	0.09347804
29	44,054,901	rs42192084	0.23271677	0.19155845	0.43966180	0.42005085	0.10259460	0.34485314
29	44,058,688	rs42192090	0.63374532	1.03088313	0.26325766	2.16293094	0.44993328	0.45997855
29	44,060,410	rs42192096	0.58111065	1.09484368	0.44353513	1.43528346	0.29247259	0.79125781
29	44,062,694	rs42192100	0.55597264	1.10606032	0.43772073	1.27617242	0.24952277	0.72058476
29	44,063,938	rs17872078	11.06385692	4.73157664	3.95490039	3.60275558	0.12298021	3.56044339
29	44,067,234	rs17872093	0.49119246	1.09484368	0.61056779	1.43528346	0.24952277	0.82128250
29	44,067,796	rs17871984	9.12386593	4.17029373	6.17311920	1.38841165	0.33534977	1.65236722
29	44,068,143	rs17870631	15.02478285	6.53020157	4.79267429	5.02153497	0.01743977	5.61780734
29	44,068,346	rs17870628	8.02478258	3.72104979	5.03083483	1.69430079	0.23008326	2.29019068
29	44,068,445	rs17870626	14.02591772	5.99882130	4.56681868	4.87245328	0.10332268	5.32147410
29	44,068,519	rs17872010	13.92040678	6.23558901	4.32611748	5.02153497	0.01743977	5.22609254
29	44,068,580	rs17872004	14.69756940	6.53020157	4.70900007	4.95672805	0.04699462	5.33363070
29	44,068,812	rs17872003	14.52861819	6.54890094	4.68559191	5.23726316	0.05731284	5.26903465
29	44,069,063	rs17812000	15.01318351	9.70325035	3.86955288	5.02153497	0.01743977	5.34387541
29	44,069,177	rs17872006	12.16297032	6.95858004	3.95278603	3.63333825	0.20827835	4.93570623
29	44,070,713	rs42192103	15.25158225	5.57498348	5.51973138	5.66567676	0.18467504	5.99674646
29	44,070,881	rs42192105	3.44303003	1.04085226	3.19416028	0.16828075	0.05476708	0.95464665
29	44,071,034	rs42192107	3.60877221	1.14058147	3.31494388	0.42816961	0.05476708	0.59604337
29	44,071,135	rs42192108	0.84761227	0.11400826	0.24937838	0.31296813	1.21868023	0.05172524
29	44,071,593	rs42192109	1.34891868	2.04739447	0.13589882	2.48998697	0.46197675	0.93864158
29	44,085,642	rs17871051	5.52314725	6.47497947	0.90205454	1.69543379	0.89215774	2.61559871
29	44,085,769	rs17871058	7.11609711	3.39328007	0.60316732	4.37345894	2.84572845	2.88941271
29	44,087,205	rs17872032	4.07412817	2.69647902	0.11119448	2.27449768	0.61567777	2.27417512
29	44,087,356	rs17872033	4.80268257	5.73921171	0.86225702	1.56598606	1.12117208	1.91960350
29	44,087,629	rs17872050	7.27411721	3.95801125	0.58442547	4.49008758	3.23458930	2.59790176
29	44,087,858	rs17872151	1.91592723	0.05811805	1.11957708	0.90851090	0.28340516	0.74334865

29	44,088,897	rs17870847	6.98857664	3.53198021	0.49906676	4.69114559	3.16712717	2.42102017
29	44,110,295	rs42192119	0.24763846	0.11219104	0.09233846	0.61056832	0.36911136	0.14787609
29	44,119,671	rs42195143	0.13149919	0.33349792	0.99637011	0.05862776	0.10126358	0.17576138
29	44,122,272	rs42194216	0.44091580	0.18173824	0.76346807	0.27321828	0.10568910	0.00595621
29	44,125,747	rs42194178	0.47074672	0.24535880	0.89696110	0.27137387	0.10568910	0.00595621
29	44,130,887	rs42194132	0.34790036	0.24535880	0.80201702	0.27822368	0.10568910	0.14103651
29	44,154,126	rs42193349	0.73134565	1.60354632	1.02285973	0.22531657	0.16005057	0.43020523
29	44,172,614	ss117965984	0.89921288	0.00903521	0.79790059	0.48422659	0.20438421	0.83691045
29	44,196,154	ss86318958	0.17826692	0.83275480	0.79139179	0.31733155	0.09584821	0.09352201
29	44,208,978	rs29003633	0.72332983	4.82095682	0.01810898	0.13778251	0.05217681	0.29638830
29	44,223,148	ss86323783	1.87225920	3.93233393	0.04523253	1.83618667	0.67743646	0.14198146
29	44,243,444	ss86313099	0.08257010	1.92540086	1.69616348	0.95541644	0.08870579	0.24639965
29	44,325,408	ss86292140	5.67467249	5.33541800	1.08931228	1.55484928	0.44966064	2.51916267
29	44,372,611	ss86329852	0.53162591	0.02803790	0.48418639	1.23731403	0.80255075	0.90485283
29	44,395,075	ss86333994	2.06219114	1.66817727	1.16265211	0.06130758	0.18184149	2.06865498
29	44,416,282	rs43709648	5.68390548	4.77448860	4.22466506	1.33513815	0.06867912	0.52090920
29	44,546,564	ss86288185	1.62442034	1.35229526	1.25855827	0.71522273	0.04494773	0.39605969
29	44,585,782	ss86341172	0.93033545	0.89359393	0.51199420	1.19185100	0.31208265	0.27979050
29	44,628,137	rs41600300	0.10219117	1.45782122	0.41298898	0.31552270	0.70959496	0.63515653
29	44,649,908	ss86337530	0.04163328	0.09909412	1.09696773	0.27955691	0.09828177	0.87398116
29	44,740,917	ss86334185	1.17528419	1.72921586	1.09441063	0.35244420	0.28055154	0.22148194
29	44,807,928	ss117965824	0.24486922	1.68461918	1.22415017	0.02552680	0.03251072	0.15375166
29	44,853,970	rs42192429	0.04285861	2.70896169	0.24443504	0.96548290	0.25802019	1.05292526
29	44,900,940	rs43706228	1.16255448	4.47829875	0.12815280	2.96298435	0.05421330	0.16986484
29	44,969,518	ss86337154	0.75559117	0.31551240	0.38456438	0.97456211	0.29136167	0.29457028
29	44,979,377	ss86338214	0.16929778	0.41243332	0.34406199	0.23475380	0.09033549	0.48360841
29	44,999,264	ss86310727	2.47136644	1.33314498	0.07862254	1.19352282	1.15758380	1.89272860
29	45,023,665	ss86338763	0.50154984	0.31551240	1.02362911	0.82814950	0.29136167	0.22855959
29	45,102,557	ss86332221	2.80208621	1.39414911	0.10735358	3.81708940	0.08121695	2.01548437
29	45,129,099	ss86335405	1.92518407	1.91040532	0.55154806	1.87871179	0.10445101	0.35823047
29	45,187,114	ss86295760	0.48656271	1.77102946	0.30303839	0.06520406	0.15318487	0.07669521

						-log ₁₀ (P)HSE ⁷		
BTA	POS ¹	SNP ID ²	H-All Breeds	H-Angus	H-Hereford	H-Charolais	H-Limousin	H-Simmental
7	97,151,592	rs41656985						
7	97,261,052	rs41656987						
7	97,372,656	rs41570922						
7	97,393,157	rs41615915						
7	97,430,691	ss86295638	0.26508076	0.22716139	0.35490286	0.11939695	1.17950014	0.05611460
7	97,501,859	ss86310801	0.81800928	0.07156966	0.33609847	0.06345397	2.15235804	0.09168065
7	97,529,872	ss61472319	1.98049919	0.14371942	1.39259947	0.12678032	1.29152534	0.15902671
7	97,691,853	ss86290016	1.38106720	0.03262946	1.44345770	0.06604644	1.08465456	0.00273854
7	97,772,240	ss86312419	1.11696273	0.03704186	0.59346134	0.01414687	1.48842612	0.51559835
7	97,861,341	rs41593284	1.07333880	0.18884830	1.54612811	1.28697105	1.94622343	0.70741950
7	97,898,940	rs41593281	1.20710768	0.21395773	0.35285888	0.56983555	0.84014096	0.97571611
7	97,961,659	ss117969141	1.56513141	0.58260066	1.18631024	0.80927320	1.45814808	0.69798479
7	98,013,150	ss117968909	1.94109221	0.42866082	1.70014361	1.07709074	1.53017736	0.54579568
7	98,173,299	ss86290989	5.19485373	0.21666189	3.08995548	0.57537080	0.40169634	1.26846310
7	98,194,828	rs41658549	7.19312845	1.45022845	3.28674164	0.88346307	0.94186821	1.09107705
7	98,254,815	rs41658542	7.30762392	1.20874235	3.86521461	0.64348316	1.16137417	1.44864297
7	98,375,640	ss86329349	5.20735013	0.69984802	3.62626557	0.21261409	0.99651092	1.49969468
7	98,495,888	rs43529872	8.78946851	2.75028009	3.88742490	3.77219492	1.18671624	0.67066205
7	98,498,047	ss86321563	5.26395768	0.95003489	3.26823256	1.24059094	0.59144138	0.50885778
7	98,538,952	rs41660170	5.75844597	1.24611419	4.18746267	4.02764991	0.34395397	1.25539145
7	98,566,391	ss117962527	5.29372661	0.80510588	4.56286232	2.37126445	0.89744762	0.24031325
7	98,579,574	rs41255587	3.98897683	0.52039442	3.44498563	2.02857191	0.63931022	0.40299644
7	98,635,208	ss86300200	2.32088832	0.36484788	3.13453957	1.47339982	1.97169891	0.04134551
7	98,646,770	rs41596489	3.35672116	0.12551053	2.35292792	0.83513958	0.61692184	0.74500295
7	98,680,293	ss86315737	1.46829182	0.45527887	1.11997405	0.72275624	1.52410372	0.77676452
7	98,726,055	rs29018251	2.68450826	0.00446483	2.59819051	1.64736930	0.04882888	1.21792070
7	98,757,265	ss86303738	0.25145766	0.01037767	1.07605607	0.11879893	0.05675627	0.52793539
7	98,820,742	ss86324113	1.27277626	0.00316008	0.87855733	0.82996525	0.16650701	0.07170139
7	98,887,313	rs41568595	1.04874555	0.24055696	1.92106638	2.27907223	0.25832342	0.34138781
7	98,907,404	ss86291843	0.12659421	0.04140937	0.47312626	1.08738269	0.30143055	0.17518428
7	98,974,456	ss86339659	0.35618278	0.11996119	0.43000780	3.20102208	1.59395272	0.16889318
7	99,024,444	ss117968912	1.38169398	0.46449100	2.42800812	3.82249522	0.33963017	0.03566803
7	99,085,299	rs41590403	1.41246704	0.22315877	2.07804148	1.22225322	0.25108351	0.12469519
7	99,130,598	ss86333606	0.46025697	0.00984278	1.09712190	0.87025315	0.99486135	0.02418621
7	99,178,748	rs41568774	0.27207244	0.07530685	0.40169694	1.03480593	0.17213830	0.08893838
7	99,215,474	ss86324013	1.54040285	0.23635459	1.69528036	0.45088169	0.01317582	0.20992227
7	99,344,820	rs41622872	0.77418023	1.10702407	0.64002365	0.03192407	0.45514191	0.44536115
7	99,399,852	ss117968895	0.02699322	0.01194669	0.05783008	0.01770490	0.62311139	0.00584030
7	99,492,904	ss86296856	0.67099476	0.03420171	0.23136372	0.31714738	0.56405439	0.21482810
7	99,635,841	ss86339853	0.26382175	0.06423947	0.07232531	0.24511858	1.09094161	0.22922627
7	99,687,614	rs41657025						
7	99,845,133	rs41624339						
7	99,919,908	ss86339607						
7	100,015,468	ss86310226						
29	42,406,544	ss86319674						
29	42,455,680	ss117974470						
29	42,620,218	rs42189770						
29	42,651,294	rs43706142						
29	42,696,595	rs42189112	0.30906697	0.88607575	0.02123152	0.39494132	0.15097430	0.23355190
29	42,749,808	rs29020063	0.60218769	0.98996223	0.03249730	0.59290246	0.34019608	1.19943101
29	42,842,353	ss117974486	1.13550193	0.65699706	0.47372237	0.02181479	0.08405313	1.12277303
29	42,897,144	ss86322358	0.71512224	2.11448646	0.53312529	0.14369412	0.21209756	0.88613922

29	43,006,000	ss86339964	0.73271265	2.41188485	0.33960364	0.08529153	0.77321440	1.56473566
29	43,043,207	ss86341572	0.82246094	2.32985985	0.11124371	0.09751926	0.15356810	1.43976778
29	43,108,445	ss86337140	0.81896949	2.33109058	0.00285613	0.00222270	0.18021498	1.69495979
29	43,129,250	ss86337549	1.63994035	4.20422145	0.06100995	0.16876456	0.03220266	0.93963329
29	43,189,370	ss86319044	1.18301713	1.19782548	0.86122390	0.01091282	0.23608231	0.49359785
29	43,224,753	rs29013208	2.37813436	3.18593611	1.67880213	0.01106032	0.11811475	0.61501851
29	43,269,744	ss86282762	3.86475938	3.82149385	2.26416192	0.14418999	0.55321311	0.92959597
29	43,304,256	rs29024708	1.24577534	1.55404902	0.83388990	0.16568222	0.13932080	1.35982228
29	43,328,607	ss86295061	1.62487690	2.40837626	0.42667436	1.64421339	0.02121940	1.33710261
29	43,429,511	ss86318094	2.12572529	3.80842344	1.28881993	0.95480642	0.02553625	1.44611500
29	43,466,342	ss86310741	0.71555522	1.12116750	0.88703677	0.33284474	0.00270686	0.56692846
29	43,498,073	ss86338800	1.45812150	2.95862003	0.90383764	0.85347409	0.41198322	0.31775444
29	43,611,640	ss86298040	1.71738830	1.49905151	0.65021301	0.56840134	0.58927359	0.81617442
29	43,652,252	ss86327310	1.85247447	2.72293599	0.38704847	1.21836700	0.46366774	1.06027271
29	43,686,401	ss86325323	2.85471722	5.50057900	0.89673711	1.10064931	0.00287942	2.04317052
29	43,709,769	ss86290081	2.37660557	7.30961397	0.69453568	0.90919636	0.76372755	2.56351112
29	43,747,765	rs42190085	1.57659695	2.45959885	0.82975654	0.08757620	0.69431647	2.26028050
29	43,749,527	ss86299346	1.17290269	1.12334737	0.87827269	0.58774448	0.69851826	1.38948401
29	43,777,249	ss86299989	3.02787309	1.34862602	1.70160346	0.33254679	1.47845730	1.58800258
29	43,826,144	rs42191289	5.32853039	1.18426692	3.31864667	0.80798556	0.11909686	1.37750458
29	43,839,783	ss86336460	0.34757971	1.24877665	0.88353443	0.25582816	0.10286128	0.42109271
29	43,914,923	ss86335514	0.41546339	0.90700286	0.13421452	0.59111298	0.14605836	0.88599779
29	44,000,728	rs42191319	0.82185269	0.04755089	0.49823042	0.84353654	0.13510732	0.83505751
29	44,029,526	rs42192038	0.50880964	0.31129890	0.27972788	0.86600833	0.26925594	0.44131506
29	44,042,363	rs42192064	0.13658017	0.11580871	0.72905363	0.71583709	0.01905937	0.08194063
29	44,049,244	rs42192077	1.35767164	1.22634702	0.85886097	1.46652883	0.02509769	0.70198908
29	44,050,471	ss86284058	1.61646995	1.67349815	0.67683014	0.48665107	0.28414395	1.97858819
29	44,051,567	rs42192079	3.30712727	1.42085559	2.44795993	0.82580793	0.00975328	2.86690989
29	44,053,733	rs42192083	3.39158339	2.38296426	1.30292318	0.94212815	0.21402334	3.00111352
29	44,054,901	rs42192084	11.49369842	3.55621855	5.21648679	3.10996361	0.23084442	1.99917782
29	44,058,688	rs42192090	7.88594584	1.80903613	5.70470916	3.31341794	0.09513478	2.83102329
29	44,060,410	rs42192096	0.12986183	1.46336669	2.16083744	1.23070016	0.45062150	0.15558495
29	44,062,694	rs42192100	12.27238874	2.41838262	6.74301670	1.67412867	0.48273454	1.60991865
29	44,063,938	rs17872078	12.23589788	2.29047402	5.87511925	2.49050918	0.10200335	2.19095222
29	44,067,234	rs17872093	16.88269453	6.57015459	5.61324508	3.26121021	0.26036723	4.51981527
29	44,067,796	rs17871984	18.42738682	5.84412338	5.71691132	4.08482900	0.27637483	4.20909177
29	44,068,143	rs17870631	18.39968289	6.37524252	5.45793276	4.05568887	0.23002304	4.03478613
29	44,068,346	rs17870628	12.38241270	5.04806672	2.70913095	4.10912997	0.24068611	2.93239801
29	44,068,445	rs17870626	13.82885695	9.34358563	3.53168518	4.15858213	0.32596470	3.28779936
29	44,068,519	rs17872010	15.25910115	9.89889309	5.93905737	4.63045660	1.24106440	3.82501971
29	44,068,580	rs17872004	6.47969623	5.68172394	3.81874178	0.49614568	0.25001902	1.82874448
29	44,068,812	rs17872003	2.05963582	2.46398596	1.24572801	1.47993935	0.15068095	0.56014166
29	44,069,063	rs17812000	9.77853894	7.47435434	2.39643816	2.79419971	0.12049838	3.66924718
29	44,069,177	rs17872006	13.46353251	7.96050207	3.86770851	4.29375576	0.88025979	3.88562500
29	44,070,713	rs42192103	11.55151331	6.44427023	4.27234495	4.12354576	0.95747805	2.99347063
29	44,070,881	rs42192105	13.20467660	6.97082267	4.74847929	5.85379933	1.34839067	2.63128615
29	44,071,034	rs42192107	12.98510976	6.43286369	4.17187350	5.64602414	0.28760212	2.92776017
29	44,071,135	rs42192108	2.37657109	2.85669709	1.57339654	0.99186327	0.28553372	0.51775051
29	44,071,593	rs42192109	2.43465244	2.35156168	1.72365835	1.06696035	0.56643274	0.11445303
29	44,085,642	rs17871051	2.22122719	3.74051691	0.20554006	3.10807112	0.97276859	2.13239684
29	44,085,769	rs17871058	6.61208861	8.38064456	3.00878845	3.07580730	1.26456466	2.23802562
29	44,087,205	rs17872032	6.40228903	7.70690103	1.37392140	1.67479791	1.32025609	2.25287170
29	44,087,356	rs17872033	2.71654734	2.41023275	0.82639683	0.30604784	1.49210014	0.98590337
29	44,087,629	rs17872050	2.98168563	1.19410286	1.05055383	1.77522158	0.83669683	1.28942592
29	44,087,858	rs17872151	1.93894476	1.14413413	1.96526756	0.39565199	0.29177155	0.62766408

29	44,088,897	rs17870847	0.16133199	0.79403792	0.21583410	0.49005619	0.02166887	0.00111337
29	44,110,295	rs42192119	1.60735942	0.87925948	0.21436998	1.12419681	0.03163904	1.06791215
29	44,119,671	rs42195143	1.22792288	0.54340136	0.97473257	0.20362366	0.10037664	0.29155327
29	44,122,272	rs42194216	2.51318370	0.47540070	1.04175576	2.70682242	0.14208366	1.16366448
29	44,125,747	rs42194178	2.23965847	0.35775641	0.18928124	2.96180470	0.07248796	1.32894979
29	44,130,887	rs42194132	1.81890816	0.46168104	0.39822265	1.67786057	0.29121497	1.17182571
29	44,154,126	rs42193349	0.65076323	3.31740232	0.02064049	0.26745156	0.31157124	0.36263333
29	44,172,614	ss117965984	0.23199661	3.28778318	1.02199034	2.44002739	0.05228876	0.36745166
29	44,196,154	ss86318958	1.81161647	1.75877838	2.16745327	0.19969184	0.01874044	1.57245625
29	44,208,978	rs29003633	1.87290255	3.00026737	0.70748339	0.12248651	0.01088652	1.10235697
29	44,223,148	ss86323783	1.54925700	0.56620010	2.55633328	0.59153503	0.02959121	1.37000248
29	44,243,444	ss86313099	1.65698290	0.89625423	2.40467619	0.64371127	0.20064084	0.76500188
29	44,325,408	ss86292140	6.82799864	1.97015854	3.23951326	2.38246215	0.32381463	0.80251350
29	44,372,611	ss86329852	1.44683209	0.19968322	2.94240217	0.12341834	0.54213787	0.50892430
29	44,395,075	ss86333994	1.43940004	0.57500362	2.98266063	0.19138583	0.46385971	0.49592585
29	44,416,282	rs43709648	1.56049570	2.54501513	1.06492009	0.63239930	0.01669722	0.90088312
29	44,546,564	ss86288185	5.32381518	3.01422973	3.84893761	0.53942642	0.00462038	1.36466524
29	44,585,782	ss86341172	2.46757085	1.31429916	0.75921234	0.64833951	0.01279982	0.53388457
29	44,628,137	rs41600300	0.59487472	2.14009510	0.49302374	0.15268886	0.55836508	0.91422243
29	44,649,908	ss86337530	1.01897824	1.15277044	0.96862457	1.32901788	0.30646495	1.12382422
29	44,740,917	ss86334185	0.48680305	2.69382778	0.26618189	0.25735165	0.12919985	0.70970398
29	44,807,928	ss117965824	2.15392065	3.50921540	0.05121356	2.63424357	0.08061088	0.55089100
29	44,853,970	rs42192429	2.31724705	5.76063374	0.77973760	0.17127986	0.80095841	0.88638095
29	44,900,940	rs43706228	2.19610799	3.93534502	1.11862283	0.39006681	0.76834606	0.28628755
29	44,969,518	ss86337154	1.94685789	5.32150326	0.59049892	1.21396124	0.34880684	0.04453270
29	44,979,377	ss86338214	0.62499693	1.76815948	0.83021256	0.35757153	0.24917828	0.37576807
29	44,999,264	ss86310727	0.58311707	0.05002567	0.40984010	1.24270857	0.16974211	0.20788783
29	45,023,665	ss86338763	1.10742450	2.82842226	0.54096063	3.35054933	0.06487693	0.47992127
29	45,102,557	ss86332221	0.70729646	1.30554383	0.40632859	3.33952068	0.20370789	0.65698242
29	45,129,099	ss86335405	0.08011029	0.56628152	0.17913265	1.47136413	0.10457292	0.03010530
29	45,187,114	ss86295760	3.90874839	0.47612537	3.19993420	1.36504297	0.10578806	0.13928507
29	45,287,502	ss86312485	1.62763739	2.77694631	2.25493961	0.77715979	0.15892100	0.81196521
29	45,326,585	rs42198683	1.84232573	2.43676900	2.15095695	1.04701284	0.35084659	0.49732541
29	45,367,095	ss86322638						
29	45,458,280	rs43706176						
29	45,482,143	rs29025626						
29	45,530,264	ss86341375						

¹UMD3.1 Coordinates. SNPs located within *CAST* and *CAPN1* are shaded in yellow.

²Commercialized SNPs are shaded in red.

³GBLUP allele substitution effect (α) ranks. Values less than 500 are shaded in yellow for the across-breed and green for the within-breed.

⁴GBLUP of SNP allele substitution effects (α) estimated as a random effect.

⁵SNP allele substitution effects (β) estimated as fixed effects in a mixed linear model including the genomic relationship matrix.

⁶ $-\log_{10}(P)$ -value for the test of the null hypothesis of an allele substitution effect (β) of zero. Maximum values are shaded in red.

⁷ $-\log_{10}(P)$ -value for the test of the null hypothesis of all haplotype substitution effects (H) being zero. Maximum values are shaded in red.

⁸Number of haplotypes and effective number of haplotypes in parentheses for the 13 (*CAST*) or 31 (*CAPN1*) SNP block centered on the identified SNP.

⁹Number Percentage of phenotypic variation in WBSF explained by haplotypes centered on the identified SNP.

						No. Haplotypes ⁸		
BTA	POS ¹	SNP ID ²	All Breeds	Angus	Hereford	Charolais	Limousin	Simmental
7	97,151,592	rs41656985						
7	97,261,052	rs41656987						
7	97,372,656	rs41570922						
7	97,393,157	rs41615915						
7	97,430,691	ss86295638	8 (2.97)	8 (2.20)	6 (2.65)	8 (3.79)	7 (3.73)	8 (2.67)
7	97,501,859	ss86310801	8 (3.65)	8 (3.13)	6 (2.76)	8 (4.47)	6 (4.83)	7 (3.52)
7	97,529,872	ss61472319	8 (3.73)	8 (3.05)	7 (3.00)	7 (3.84)	7 (4.44)	8 (3.78)
7	97,691,853	ss86290016	7 (3.89)	7 (3.07)	6 (2.99)	7 (4.04)	7 (4.55)	7 (4.19)
7	97,772,240	ss86312419	7 (3.57)	7 (2.77)	7 (2.85)	7 (4.57)	7 (4.61)	7 (3.72)
7	97,861,341	rs41593284	7 (3.04)	7 (2.07)	6 (2.42)	7 (3.99)	7 (5.29)	7 (3.18)
7	97,898,940	rs41593281	6 (3.46)	6 (2.90)	6 (2.45)	6 (4.16)	6 (4.23)	6 (4.06)
7	97,961,659	ss117969141	6 (3.22)	6 (3.22)	5 (1.95)	6 (3.62)	6 (3.74)	6 (4.00)
7	98,013,150	ss117968909	7 (3.41)	6 (3.31)	5 (2.07)	7 (4.01)	6 (3.86)	6 (4.13)
7	98,173,299	ss86290989	8 (4.77)	6 (3.82)	7 (3.56)	7 (4.07)	6 (4.22)	8 (4.02)
7	98,194,828	rs41658549	8 (4.43)	6 (3.27)	7 (3.54)	6 (3.95)	6 (3.97)	8 (3.53)
7	98,254,815	rs41658542	8 (4.34)	7 (3.52)	7 (3.42)	6 (4.03)	7 (4.29)	8 (3.65)
7	98,375,640	ss86329349	8 (4.18)	7 (3.20)	7 (3.63)	7 (3.42)	7 (3.84)	8 (3.60)
7	98,495,888	rs43529872	9 (4.21)	8 (3.39)	8 (3.34)	7 (3.38)	8 (3.95)	9 (3.46)
7	98,498,047	ss86321563	9 (5.03)	8 (3.93)	8 (3.79)	8 (4.01)	8 (4.51)	9 (3.92)
7	98,538,952	rs41660170	8 (4.20)	8 (3.58)	7 (2.97)	8 (3.90)	7 (3.46)	8 (4.00)
7	98,566,391	ss117962527	8 (3.78)	8 (3.22)	6 (2.79)	7 (3.61)	6 (3.01)	7 (4.49)
7	98,579,574	rs41255587	8 (4.10)	8 (2.92)	6 (3.20)	7 (3.98)	6 (3.23)	7 (4.40)
7	98,635,208	ss86300200	8 (3.25)	8 (3.00)	6 (2.70)	7 (3.35)	6 (2.89)	7 (3.34)
7	98,646,770	rs41596489	9 (3.46)	9 (3.75)	6 (2.50)	7 (4.01)	6 (3.07)	7 (3.17)
7	98,680,293	ss86315737	8 (3.54)	8 (3.48)	6 (2.82)	7 (4.08)	7 (3.31)	7 (3.38)
7	98,726,055	rs29018251	8 (3.54)	7 (3.63)	7 (2.66)	7 (3.66)	7 (3.73)	8 (3.41)
7	98,757,265	ss86303738	7 (3.38)	6 (4.02)	5 (2.52)	7 (3.81)	6 (3.12)	7 (3.29)
7	98,820,742	ss86324113	7 (4.01)	7 (3.97)	7 (2.93)	6 (3.86)	6 (3.56)	7 (3.45)
7	98,887,313	rs41568595	8 (4.84)	7 (4.79)	7 (4.12)	7 (4.98)	7 (3.89)	8 (4.53)
7	98,907,404	ss86291843	7 (4.35)	6 (3.78)	6 (3.51)	7 (4.39)	7 (3.50)	7 (4.70)
7	98,974,456	ss86339659	7 (3.79)	7 (3.93)	7 (3.15)	7 (4.04)	7 (2.91)	7 (3.89)
7	99,024,444	ss117968912	7 (3.58)	7 (3.19)	6 (3.30)	7 (3.37)	6 (3.41)	6 (3.47)
7	99,085,299	rs41590403	7 (3.97)	6 (3.54)	6 (3.77)	6 (3.61)	6 (3.06)	7 (4.21)
7	99,130,598	ss86333606	7 (3.89)	6 (3.51)	6 (3.62)	6 (3.70)	6 (3.64)	7 (4.08)
7	99,178,748	rs41568774	9 (4.42)	7 (4.37)	6 (3.60)	6 (3.92)	6 (3.95)	8 (4.52)
7	99,215,474	ss86324013	9 (4.14)	7 (4.41)	8 (3.25)	7 (4.05)	7 (3.59)	9 (4.71)
7	99,344,820	rs41622872	8 (3.77)	6 (4.34)	8 (2.69)	7 (3.64)	7 (3.45)	8 (4.05)
7	99,399,852	ss117968895	9 (3.71)	7 (3.58)	8 (3.08)	6 (3.31)	7 (3.36)	7 (4.11)
7	99,492,904	ss86296856	8 (4.87)	7 (4.59)	7 (3.06)	6 (4.06)	7 (3.43)	7 (4.87)
7	99,635,841	ss86339853	9 (4.28)	7 (4.79)	7 (2.39)	7 (4.52)	8 (3.65)	7 (4.39)
7	99,687,614	rs41657025						
7	99,845,133	rs41624339						
7	99,919,908	ss86339607						
7	100,015,468	ss86310226						
29	42,406,544	ss86319674						
29	42,455,680	ss117974470						
29	42,620,218	rs42189770						
29	42,651,294	rs43706142						
29	42,696,595	rs42189112	7 (3.96)	7 (3.83)	7 (3.14)	7 (3.75)	7 (4.05)	7 (3.91)
29	42,749,808	rs29020063	8 (5.15)	8 (4.64)	8 (4.10)	8 (4.93)	8 (4.67)	8 (5.59)
29	42,842,353	ss117974486	9 (4.30)	8 (3.29)	9 (4.15)	8 (3.99)	8 (4.62)	9 (4.81)
29	42,897,144	ss86322358	9 (4.91)	9 (3.94)	9 (3.93)	9 (4.52)	9 (5.42)	9 (4.80)

29	43,006,000	ss86339964	10 (3.56)	9 (3.28)	9 (3.08)	9 (2.93)	9 (5.55)	10 (4.31)
29	43,043,207	ss86341572	9 (3.80)	8 (3.87)	8 (2.50)	8 (3.66)	8 (4.67)	9 (4.61)
29	43,108,445	ss86337140	10 (2.88)	7 (2.57)	7 (2.26)	7 (2.72)	7 (4.72)	10 (3.45)
29	43,129,250	ss86337549	9 (2.36)	7 (2.21)	7 (1.92)	7 (2.38)	6 (3.65)	9 (2.67)
29	43,189,370	ss86319044	8 (2.25)	7 (2.21)	7 (1.63)	7 (2.50)	7 (3.07)	8 (3.07)
29	43,224,753	rs29013208	8 (2.92)	6 (2.71)	7 (2.68)	7 (2.61)	6 (3.06)	8 (3.35)
29	43,269,744	ss86282762	7 (2.83)	5 (2.57)	6 (2.86)	6 (2.66)	6 (1.80)	7 (3.23)
29	43,304,256	rs29024708	7 (3.26)	5 (3.05)	7 (3.04)	6 (3.16)	5 (2.25)	7 (3.62)
29	43,328,607	ss86295061	7 (4.00)	7 (3.65)	5 (3.71)	6 (4.22)	5 (3.17)	7 (3.83)
29	43,429,511	ss86318094	8 (4.72)	8 (4.52)	6 (3.85)	7 (5.13)	6 (3.17)	8 (4.74)
29	43,466,342	ss86310741	8 (5.38)	7 (4.56)	7 (5.75)	6 (5.46)	7 (3.18)	8 (5.07)
29	43,498,073	ss86338800	8 (6.21)	8 (6.12)	8 (6.03)	7 (6.12)	7 (3.37)	8 (6.18)
29	43,611,640	ss86298040	9 (6.18)	8 (5.89)	8 (5.38)	9 (6.26)	7 (3.47)	8 (6.39)
29	43,652,252	ss86327310	7 (5.32)	7 (6.32)	7 (3.74)	7 (5.34)	7 (3.61)	7 (6.21)
29	43,686,401	ss86325323	7 (5.06)	6 (4.83)	6 (4.88)	7 (5.03)	6 (4.20)	6 (4.67)
29	43,709,769	ss86290081	7 (4.64)	6 (4.69)	6 (3.82)	7 (4.94)	6 (4.33)	6 (4.83)
29	43,747,765	rs42190085	7 (4.82)	7 (5.00)	7 (2.85)	7 (5.67)	7 (4.82)	7 (5.78)
29	43,749,527	ss86299346	7 (4.47)	6 (5.42)	6 (2.75)	7 (5.42)	7 (3.53)	7 (5.49)
29	43,777,249	ss86299989	6 (4.53)	6 (4.94)	5 (3.06)	6 (4.70)	6 (3.13)	6 (4.50)
29	43,826,144	rs42191289	6 (4.42)	6 (4.50)	6 (4.17)	6 (3.93)	6 (3.55)	6 (4.53)
29	43,839,783	ss86336460	7 (4.67)	6 (4.35)	7 (4.21)	6 (4.43)	6 (3.70)	7 (4.60)
29	43,914,923	ss86335514	8 (4.57)	7 (4.10)	7 (3.53)	7 (4.69)	6 (4.87)	8 (4.86)
29	44,000,728	rs42191319	8 (4.52)	7 (4.03)	7 (4.33)	6 (4.39)	6 (4.59)	6 (4.30)
29	44,029,526	rs42192038	7 (3.76)	7 (3.19)	7 (3.53)	7 (3.70)	6 (4.11)	7 (3.44)
29	44,042,363	rs42192064	7 (3.22)	6 (2.55)	6 (2.95)	5 (3.11)	5 (4.09)	5 (3.43)
29	44,049,244	rs42192077	6 (3.30)	5 (2.98)	6 (3.08)	4 (3.34)	4 (3.04)	5 (3.32)
29	44,050,471	ss86284058	6 (3.66)	6 (3.10)	6 (3.14)	6 (3.50)	6 (2.36)	6 (3.44)
29	44,051,567	rs42192079	6 (3.10)	6 (2.97)	5 (2.85)	5 (3.26)	4 (2.30)	6 (2.95)
29	44,053,733	rs42192083	6 (3.14)	6 (2.88)	5 (2.91)	5 (3.30)	4 (3.03)	6 (3.17)
29	44,054,901	rs42192084	6 (2.71)	6 (2.42)	5 (2.46)	5 (2.88)	4 (2.29)	6 (2.92)
29	44,058,688	rs42192090	5 (2.17)	5 (2.64)	5 (1.68)	5 (2.39)	4 (1.91)	4 (2.24)
29	44,060,410	rs42192096	6 (2.07)	4 (2.28)	5 (1.51)	6 (2.39)	5 (2.04)	5 (2.70)
29	44,062,694	rs42192100	6 (1.87)	5 (1.62)	6 (1.67)	5 (2.21)	5 (1.63)	6 (2.45)
29	44,063,938	rs17872078	7 (3.06)	5 (3.19)	7 (2.19)	5 (3.33)	6 (2.84)	6 (3.61)
29	44,067,234	rs17872093	7 (3.22)	6 (2.81)	7 (2.57)	6 (3.80)	6 (2.67)	6 (3.97)
29	44,067,796	rs17871984	8 (3.00)	7 (2.79)	8 (2.45)	7 (3.31)	7 (2.14)	7 (4.12)
29	44,068,143	rs17870631	9 (2.95)	7 (2.76)	8 (2.45)	7 (3.27)	6 (2.11)	8 (3.78)
29	44,068,346	rs17870628	9 (2.09)	7 (2.44)	7 (1.58)	6 (2.29)	5 (1.68)	8 (2.57)
29	44,068,445	rs17870626	7 (1.79)	7 (2.34)	6 (1.47)	6 (1.80)	4 (1.56)	6 (1.88)
29	44,068,519	rs17872010	7 (2.87)	6 (2.98)	6 (2.39)	7 (3.04)	6 (2.14)	6 (3.35)
29	44,068,580	rs17872004	6 (1.85)	6 (2.27)	6 (1.54)	5 (1.78)	6 (1.66)	5 (2.04)
29	44,068,812	rs17872003	6 (1.42)	5 (1.52)	6 (1.41)	5 (1.35)	6 (1.28)	6 (1.51)
29	44,069,063	rs17812000	7 (1.81)	5 (2.37)	6 (1.55)	5 (1.68)	5 (1.48)	7 (1.94)
29	44,069,177	rs17872006	6 (2.40)	5 (2.81)	6 (2.38)	5 (2.40)	6 (1.78)	6 (1.98)
29	44,070,713	rs42192103	8 (3.14)	7 (3.26)	7 (2.99)	7 (3.00)	8 (2.16)	8 (2.99)
29	44,070,881	rs42192105	9 (4.11)	8 (3.75)	8 (3.22)	8 (4.32)	8 (3.14)	9 (4.12)
29	44,071,034	rs42192107	9 (5.26)	8 (4.70)	8 (3.85)	8 (5.55)	8 (4.26)	9 (5.45)
29	44,071,135	rs42192108	9 (4.51)	8 (4.05)	7 (3.83)	7 (3.50)	9 (4.44)	8 (4.09)
29	44,071,593	rs42192109	8 (3.86)	8 (3.84)	6 (3.54)	7 (3.19)	8 (2.63)	7 (3.44)
29	44,085,642	rs17871051	8 (3.97)	8 (3.91)	6 (3.27)	6 (3.65)	7 (3.31)	7 (4.06)
29	44,085,769	rs17871058	7 (4.11)	7 (3.61)	6 (3.52)	6 (3.60)	6 (3.90)	6 (4.06)
29	44,087,205	rs17872032	7 (2.73)	6 (2.16)	5 (2.41)	6 (2.80)	6 (2.49)	6 (3.11)
29	44,087,356	rs17872033	7 (3.33)	7 (2.69)	6 (3.23)	6 (3.11)	6 (3.69)	7 (3.57)
29	44,087,629	rs17872050	7 (3.16)	6 (3.00)	6 (2.79)	6 (3.32)	5 (3.73)	7 (3.14)
29	44,087,858	rs17872151	7 (2.86)	7 (2.96)	6 (2.69)	6 (2.88)	5 (3.20)	7 (2.69)

29	44,088,897	rs17870847	7 (3.41)	6 (2.81)	6 (3.30)	6 (3.61)	6 (3.93)	7 (3.11)	
29	44,110,295	rs42192119	6 (3.29)	6 (2.70)	5 (2.96)	5 (3.80)	5 (3.73)	6 (3.14)	
29	44,119,671	rs42195143	6 (2.73)	5 (2.50)	5 (2.91)	5 (2.66)	5 (3.19)	6 (2.33)	
29	44,122,272	rs42194216	6 (3.40)	5 (2.63)	6 (3.39)	6 (3.36)	6 (3.65)	6 (3.20)	
29	44,125,747	rs42194178	6 (3.53)	6 (2.80)	6 (3.64)	6 (3.54)	6 (3.56)	6 (3.22)	
29	44,130,887	rs42194132	7 (3.30)	5 (2.59)	5 (3.65)	6 (3.38)	5 (3.42)	7 (3.05)	
29	44,154,126	rs42193349	7 (3.43)	6 (2.85)	6 (3.07)	7 (3.84)	6 (3.38)	7 (3.97)	
29	44,172,614	ss117965984	7 (3.38)	5 (2.73)	5 (3.23)	7 (3.34)	6 (2.57)	6 (3.61)	
29	44,196,154	ss86318958	7 (3.43)	5 (3.27)	5 (3.29)	6 (3.29)	6 (2.81)	6 (3.56)	
29	44,208,978	rs29003633	8 (3.58)	6 (3.65)	6 (3.21)	7 (3.24)	7 (3.19)	6 (3.63)	
29	44,223,148	ss86323783	8 (3.87)	7 (3.61)	7 (2.87)	7 (3.90)	8 (4.32)	7 (4.22)	
29	44,243,444	ss86313099	8 (4.51)	8 (3.85)	8 (3.91)	8 (3.93)	8 (4.86)	8 (4.48)	
29	44,325,408	ss86292140	8 (3.88)	8 (2.40)	8 (3.56)	8 (4.31)	8 (4.87)	8 (4.02)	
29	44,372,611	ss86329852	8 (3.84)	7 (3.23)	8 (3.51)	7 (4.19)	7 (4.60)	7 (3.80)	
29	44,395,075	ss86333994	8 (3.87)	7 (3.25)	8 (3.61)	7 (4.23)	7 (4.71)	7 (3.86)	
29	44,416,282	rs43709648	8 (4.31)	7 (3.21)	8 (3.88)	8 (5.07)	7 (4.95)	8 (4.50)	
29	44,546,564	ss86288185	8 (4.92)	7 (4.21)	7 (4.75)	8 (5.14)	8 (4.49)	8 (4.64)	
29	44,585,782	ss86341172	9 (3.72)	8 (2.79)	8 (4.09)	8 (3.58)	9 (4.63)	9 (3.25)	
29	44,628,137	rs41600300	9 (4.29)	8 (3.15)	8 (4.14)	8 (3.57)	9 (4.53)	9 (3.86)	
29	44,649,908	ss86337530	8 (4.23)	6 (3.25)	8 (3.98)	7 (4.06)	7 (4.28)	8 (3.60)	
29	44,740,917	ss86334185	8 (3.53)	7 (3.16)	7 (2.90)	7 (3.23)	7 (3.91)	8 (3.46)	
29	44,807,928	ss117965824	8 (3.56)	8 (2.83)	7 (2.99)	7 (3.54)	7 (4.67)	8 (4.23)	
29	44,853,970	rs42192429	7 (4.05)	7 (4.15)	7 (3.07)	7 (4.22)	7 (4.08)	7 (4.47)	
29	44,900,940	rs43706228	8 (4.12)	8 (4.04)	7 (3.13)	8 (4.32)	7 (4.58)	8 (4.25)	
29	44,969,518	ss86337154	8 (4.45)	8 (4.24)	8 (3.82)	8 (4.46)	7 (4.60)	8 (4.57)	
29	44,979,377	ss86338214	7 (4.14)	7 (3.79)	7 (4.21)	7 (3.71)	6 (4.61)	7 (4.08)	
29	44,999,264	ss86310727	7 (3.92)	7 (3.51)	7 (2.74)	6 (3.27)	6 (3.90)	7 (4.34)	
29	45,023,665	ss86338763	7 (4.03)	6 (3.94)	7 (3.90)	6 (3.19)	6 (4.38)	7 (4.21)	
29	45,102,557	ss86332221	7 (3.53)	7 (3.34)	7 (2.88)	7 (3.65)	7 (4.83)	7 (3.92)	
29	45,129,099	ss86335405	7 (4.16)	7 (4.25)	6 (3.72)	6 (4.41)	6 (3.77)	7 (4.25)	
29	45,187,114	ss86295760	6 (4.30)	6 (3.97)	6 (3.68)	6 (4.83)	5 (3.52)	6 (4.10)	
29	45,287,502	ss86312485	6 (4.45)	6 (3.35)	6 (3.93)	6 (4.76)	6 (3.23)	6 (4.87)	
29	45,326,585	rs42198683	7 (4.08)	6 (3.24)	5 (3.51)	6 (4.34)	5 (3.09)	6 (4.52)	
29	45,367,095	ss86322638							
29	45,458,280	rs43706176							
29	45,482,143	rs29025626							
29	45,530,264	ss86341375							
¹ UMD3.1 Coordinates. SNPs located within <i>CAST</i> and <i>CAPN1</i> are shaded in yellow.									

						% V _p explained ⁹				
BTA	POS ¹	SNP ID ²	All Breeds	Angus	Hereford	Charolais	Limousin	Simmental		
7	97,151,592	rs41656985								
7	97,261,052	rs41656987								
7	97,372,656	rs41570922								
7	97,393,157	rs41615915								
7	97,430,691	ss86295638	0.1069	0.3348	0.3181	0.2968	2.9028	0.5612		
7	97,501,859	ss86310801	0.1916	0.2039	0.3081	0.2291	3.8762	0.5472		
7	97,529,872	ss61472319	0.3281	0.2727	0.8707	0.2474	3.0739	0.8633		
7	97,691,853	ss86290016	0.2342	0.1155	0.7879	0.1839	2.7549	0.1346		
7	97,772,240	ss86312419	0.2042	0.1218	0.5156	0.0972	3.3667	1.3058		
7	97,861,341	rs41593284	0.1991	0.2543	0.8272	0.8832	4.0170	1.5665		
7	97,898,940	rs41593281	0.1880	0.2159	0.3170	0.4538	2.0289	1.6484		
7	97,961,659	ss117969141	0.2257	0.3903	0.5856	0.5680	2.9404	1.3240		
7	98,013,150	ss117968909	0.2944	0.3231	0.7719	0.7887	3.0408	1.1337		
7	98,173,299	ss86290989	0.6082	0.2174	1.5111	0.5415	1.2811	2.2421		
7	98,194,828	rs41658549	0.7887	0.7155	1.5810	0.6017	2.1868	2.0381		
7	98,254,815	rs41658542	0.8412	0.7193	1.7833	0.4899	2.8748	2.7163		
7	98,375,640	ss86329349	0.6480	0.5146	1.7002	0.3179	2.6146	2.7748		
7	98,495,888	rs43529872	1.0168	1.3608	1.9218	1.8626	3.2645	1.9619		
7	98,498,047	ss86321563	0.6907	0.6996	1.6994	0.9652	2.2145	1.7102		
7	98,538,952	rs41660170	0.6994	0.8205	1.8942	2.0957	1.4259	2.4906		
7	98,566,391	ss117962527	0.6561	0.6368	1.8793	1.3322	2.1184	0.8685		
7	98,579,574	rs41255587	0.5320	0.5029	1.5045	1.1954	1.7032	1.1394		
7	98,635,208	ss86300200	0.3645	0.4199	1.3981	0.9644	3.6388	0.3863		
7	98,646,770	rs41596489	0.5032	0.3066	1.1240	0.6743	1.6654	1.6151		
7	98,680,293	ss86315737	0.2711	0.4693	0.6606	0.6184	3.4188	1.6557		
7	98,726,055	rs29018251	0.4022	0.0532	1.3334	1.0384	0.5667	2.4458		
7	98,757,265	ss86303738	0.0872	0.0489	0.5442	0.2399	0.4469	1.3233		
7	98,820,742	ss86324113	0.2221	0.0468	0.6508	0.5775	0.7773	0.4901		
7	98,887,313	rs41568595	0.2211	0.2870	1.0798	1.2957	1.2288	1.2300		
7	98,907,404	ss86291843	0.0623	0.0927	0.3782	0.7934	1.3305	0.7421		
7	98,974,456	ss86339659	0.1047	0.2045	0.4300	1.6508	3.5200	0.7290		
7	99,024,444	ss117968912	0.2343	0.4070	1.1508	1.8810	1.1603	0.2613		
7	99,085,299	rs41590403	0.2377	0.2211	1.0249	0.7492	0.9754	0.6307		
7	99,130,598	ss86333606	0.1205	0.0478	0.6514	0.5958	2.2676	0.3095		
7	99,178,748	rs41568774	0.1257	0.1654	0.3425	0.6688	0.7915	0.6747		
7	99,215,474	ss86324013	0.3063	0.2844	1.0966	0.4720	0.3325	1.1453		
7	99,344,820	rs41622872	0.1857	0.5936	0.6192	0.1349	1.6586	1.4045		
7	99,399,852	ss117968895	0.0522	0.0772	0.2063	0.0734	1.9788	0.1781		
7	99,492,904	ss86296856	0.1716	0.1178	0.3100	0.3185	1.8695	0.8208		
7	99,635,841	ss86339853	0.1240	0.1541	0.1788	0.3416	3.1080	0.8480		
7	99,687,614	rs41657025								
7	99,845,133	rs41624339								
7	99,919,908	ss86339607								
7	100,015,468	ss86310226								
29	42,406,544	ss86319674								
29	42,455,680	ss117974470								
29	42,620,218	rs42189770								
29	42,651,294	rs43706142								
29	42,696,595	rs42189112	0.0971	0.5927	0.1067	0.4390	0.9426	0.8560		
29	42,749,808	rs29020063	0.1618	0.7164	0.1655	0.6353	1.6734	2.4237		
29	42,842,353	ss117974486	0.2566	0.5694	0.6020	0.1532	0.9007	2.5806		
29	42,897,144	ss86322358	0.1998	1.2397	0.6377	0.3813	1.5694	2.2685		

29	43,006,000	ss86339964	0.2243	1.3464	0.5149	0.3115	2.8678	3.3851		
29	43,043,207	ss86341572	0.2150	1.2177	0.2691	0.2727	1.1606	2.9719		
29	43,108,445	ss86337140	0.2371	1.1154	0.0496	0.0485	1.0267	3.5414		
29	43,129,250	ss86337549	0.3180	1.7102	0.1659	0.2836	0.3402	2.3409		
29	43,189,370	ss86319044	0.2375	0.7152	0.6429	0.0879	1.1739	1.4806		
29	43,224,753	rs29013208	0.3705	1.2772	0.9855	0.0883	0.6477	1.6622		
29	43,269,744	ss86282762	0.4843	1.3414	1.0922	0.2052	1.5560	1.8456		
29	43,304,256	rs29024708	0.2190	0.6515	0.6304	0.2211	0.5122	2.3447		
29	43,328,607	ss86295061	0.2609	1.1412	0.2814	0.9226	0.1729	2.3193		
29	43,429,511	ss86318094	0.3438	1.7052	0.7278	0.7317	0.3052	2.7134		
29	43,466,342	ss86310741	0.1778	0.6858	0.6546	0.3277	0.1834	1.5918		
29	43,498,073	ss86338800	0.2699	1.4302	0.7505	0.6832	1.5707	1.1878		
29	43,611,640	ss86298040	0.3270	0.9183	0.6246	0.7037	1.9166	1.9407		
29	43,652,252	ss86327310	0.2851	1.2446	0.4059	0.8527	1.6756	2.0019		
29	43,686,401	ss86325323	0.3868	1.9641	0.5687	0.7995	0.1161	2.7630		
29	43,709,769	ss86290081	0.3391	2.4762	0.4812	0.7101	1.9074	3.2671		
29	43,747,765	rs42190085	0.2557	1.1582	0.6285	0.2086	2.1066	3.2947		
29	43,749,527	ss86299346	0.2107	0.5996	0.5609	0.5481	2.1140	2.3776		
29	43,777,249	ss86299989	0.3691	0.6800	0.7725	0.3275	2.9688	2.3050		
29	43,826,144	rs42191289	0.5797	0.6216	1.4613	0.5674	0.6505	2.0858		
29	43,839,783	ss86336460	0.1034	0.6447	0.6530	0.2815	0.6028	1.1670		
29	43,914,923	ss86335514	0.1333	0.6012	0.2374	0.5500	0.7245	2.0326		
29	44,000,728	rs42191319	0.1921	0.1353	0.4667	0.5837	0.6951	1.4871		
29	44,029,526	rs42192038	0.1275	0.3279	0.3417	0.6893	1.0148	1.1975		
29	44,042,363	rs42192064	0.0646	0.1550	0.4965	0.4318	0.1630	0.2726		
29	44,049,244	rs42192077	0.2041	0.5438	0.5527	0.6122	0.0954	1.0924		
29	44,050,471	ss86284058	0.2310	0.7920	0.4733	0.4115	1.0465	2.6991		
29	44,051,567	rs42192079	0.3953	0.7053	1.0313	0.4786	0.0496	3.5538		
29	44,053,733	rs42192083	0.4032	1.0252	0.6287	0.5270	0.4525	3.6792		
29	44,054,901	rs42192084	1.1142	1.3904	1.9370	1.3357	0.4794	2.7195		
29	44,058,688	rs42192090	0.7568	0.7332	2.0917	1.4072	0.2471	2.7775		
29	44,060,410	rs42192096	0.0489	0.5181	0.9330	0.7528	1.0922	0.4018		
29	44,062,694	rs42192100	1.1801	0.9229	2.5851	0.8142	1.1448	2.3275		
29	44,063,938	rs17872078	1.2277	0.8836	2.4599	1.1151	0.6002	2.9079		
29	44,067,234	rs17872093	1.6207	2.2689	2.3735	1.5350	0.9956	5.0523		
29	44,067,796	rs17871984	1.8030	2.1985	2.5524	1.9766	1.2721	5.1526		
29	44,068,143	rs17870631	1.8519	2.3525	2.4650	1.9660	0.9285	5.3481		
29	44,068,346	rs17870628	1.3353	1.9642	1.3739	1.8383	0.7218	4.2853		
29	44,068,445	rs17870626	1.3634	3.1851	1.5340	1.8558	0.6257	3.9445		
29	44,068,519	rs17872010	1.4843	3.1839	2.3279	2.1726	2.6316	4.4334		
29	44,068,580	rs17872004	0.6819	2.0162	1.6311	0.3337	0.9731	2.2337		
29	44,068,812	rs17872003	0.2756	0.9369	0.7108	0.7401	0.7367	1.1522		
29	44,069,063	rs17812000	1.0159	2.3693	1.1396	1.2239	0.4688	4.6553		
29	44,069,177	rs17872006	1.2804	2.5017	1.6476	1.7458	2.0917	4.4879		
29	44,070,713	rs42192103	1.2167	2.3723	1.9232	1.9906	2.8836	4.3459		
29	44,070,881	rs42192105	1.4070	2.6580	2.2227	2.7550	3.5215	4.2918		
29	44,071,034	rs42192107	1.3879	2.5015	2.0222	2.6817	1.5437	4.5974		
29	44,071,135	rs42192108	0.4005	1.3964	0.9437	0.7492	1.7837	1.5178		
29	44,071,593	rs42192109	0.3764	1.2252	0.8942	0.7841	2.1647	0.6059		
29	44,085,642	rs17871051	0.3539	1.6836	0.2326	1.4792	2.5763	3.1650		
29	44,085,769	rs17871058	0.7367	2.9196	1.3546	1.4674	2.6655	2.9538		
29	44,087,205	rs17872032	0.7179	2.5865	0.6547	0.9348	2.7454	2.9682		
29	44,087,356	rs17872033	0.3732	1.1418	0.5388	0.3120	2.9878	1.9136		
29	44,087,629	rs17872050	0.3993	0.6251	0.6325	0.9748	1.6848	2.2658		
29	44,087,858	rs17872151	0.2942	0.6947	0.9837	0.3630	0.8176	1.4608		

29	44,088,897	rs17870847	0.0699	0.4757	0.2390	0.4133	0.2829	0.0973		
29	44,110,295	rs42192119	0.2301	0.5087	0.1788	0.6008	0.2157	1.7515		
29	44,119,671	rs42195143	0.1902	0.3015	0.5057	0.1852	0.4199	0.7790		
29	44,122,272	rs42194216	0.3200	0.2749	0.6289	1.3313	0.7139	1.8567		
29	44,125,747	rs42194178	0.2934	0.2900	0.2223	1.4256	0.5045	2.0344		
29	44,130,887	rs42194132	0.2816	0.2694	0.2685	0.9360	0.8166	2.1318		
29	44,154,126	rs42193349	0.1469	1.3176	0.0735	0.3572	1.1035	1.0763		
29	44,172,614	ss117965984	0.0837	1.1845	0.5237	1.3592	0.4293	0.8918		
29	44,196,154	ss86318958	0.2808	0.7172	0.9353	0.2450	0.2646	2.2890		
29	44,208,978	rs29003633	0.3164	1.2198	0.4870	0.2434	0.3088	1.7895		
29	44,223,148	ss86323783	0.2804	0.4551	1.3181	0.5502	0.6021	2.3560		
29	44,243,444	ss86313099	0.2925	0.6766	1.3772	0.6640	1.3068	1.8720		
29	44,325,408	ss86292140	0.7977	1.0914	1.6889	1.4586	1.6338	1.9225		
29	44,372,611	ss86329852	0.2686	0.2614	1.5797	0.2443	1.8282	1.2962		
29	44,395,075	ss86333994	0.2678	0.4591	1.5946	0.3017	1.6760	1.2776		
29	44,416,282	rs43709648	0.2816	1.1864	0.8254	0.6576	0.3649	2.0519		
29	44,546,564	ss86288185	0.6589	1.3387	1.7776	0.6043	0.3169	2.6192		
29	44,585,782	ss86341172	0.4103	0.8473	0.6801	0.6665	0.5738	1.7507		
29	44,628,137	rs41600300	0.1818	1.1516	0.5392	0.3301	2.4348	2.3067		
29	44,649,908	ss86337530	0.2174	0.6102	0.7810	0.9018	1.3420	2.3320		
29	44,740,917	ss86334185	0.1446	1.2352	0.3330	0.3502	0.8755	1.7962		
29	44,807,928	ss117965824	0.3468	1.6097	0.1538	1.4348	0.7054	1.5679		
29	44,853,970	rs42192429	0.3331	2.1742	0.6054	0.2857	2.2915	1.7928		
29	44,900,940	rs43706228	0.3513	1.7453	0.7563	0.5117	2.2357	1.1298		
29	44,969,518	ss86337154	0.3245	2.1719	0.5930	0.9527	1.4366	0.5132		
29	44,979,377	ss86338214	0.1435	0.9229	0.6287	0.4160	0.9712	1.0971		
29	44,999,264	ss86310727	0.1378	0.1383	0.4188	0.7578	0.7855	0.8074		
29	45,023,665	ss86338763	0.2031	1.1662	0.4889	1.5674	0.4774	1.2544		
29	45,102,557	ss86332221	0.1543	0.7558	0.4168	1.7026	1.0905	1.5001		
29	45,129,099	ss86335405	0.0505	0.4551	0.2156	0.8526	0.6079	0.3385		
29	45,187,114	ss86295760	0.4511	0.3444	1.4206	0.8089	0.4334	0.5176		
29	45,287,502	ss86312485	0.2321	1.1501	1.0889	0.5532	0.7580	1.4601		
29	45,326,585	rs42198683	0.2840	1.0424	0.9296	0.6741	0.9232	1.0704		
29	45,367,095	ss86322638								
29	45,458,280	rs43706176								
29	45,482,143	rs29025626								
29	45,530,264	ss86341375								

¹UMD3.1 Coordinates. SNPs located within *CAST* and *CAPN1* are shaded in yellow.

²Commercialized SNPs are shaded in red.

³GBLUP allele substitution effect (α) ranks. Values less than 500 are shaded in yellow for the across-breed and green for the within-breed

⁴GBLUP of SNP allele substitution effects (α) estimated as a random effect.

⁵SNP allele substitution effects (β) estimated as fixed effects in a mixed linear model including the genomic relationship matrix.

⁶ $-\log_{10}(P)$ -value for the test of the null hypothesis of an allele substitution effect (β) of zero. Maximum values are shaded in red. Other large

⁷ $-\log_{10}(P)$ -value for the test of the null hypothesis of all haplotype substitution effects (H) being zero. Maximum values are shaded in red.

⁸Number of haplotypes and effective number of haplotypes in parentheses for the 13 (*CAST*) or 31 (*CAPN1*) SNP block centered on the identified

⁹Number Percentage of phenotypic variation in WBSF explained by haplotypes centered on the identified SNP.

[illegible]

[illegible]

[illegible]